

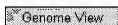
BLAST Basic Local Alignment Search Tool

Job Title: X70683:H.sapiens mRNA for SOX-4 protein

[Please, try our new design!](#)

BLASTN 2.2.18+

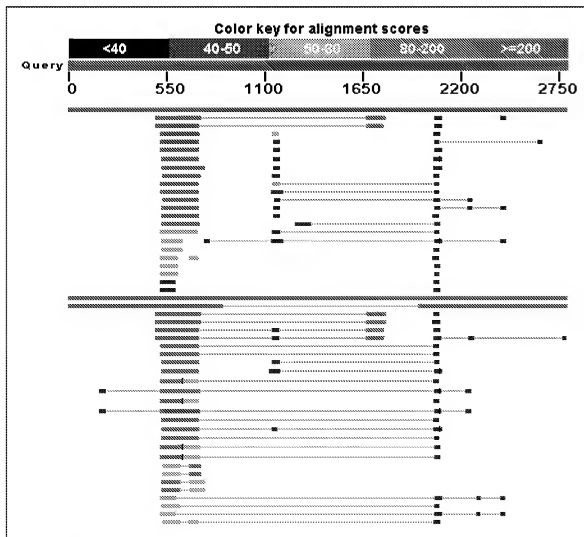
Reference: Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402. RID: 7WFM2732012 Database: human build 36.3 reference assembly genomic scaffolds 49,942 sequences; 5,818,011,736 total letters



Show positions of the BLAST hits in the human genome using the Entrez Genomes MapViewer

Query= gi|36552|emb|X70683.1|HSSOX4M H.sapiens mRNA for SOX-4 protein Length=2797

Distribution of 270 Blast Hits on the Query Sequence



2000000-2000000
2000000-2000000
2000000-2000000
2000000-2000000
2000000-2000000

Distance tree of results **NEW**Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **M** Map ViewerSequences producing significant alignments:
(Click headers to sort columns)

Transcripts

NM_003107.2	Homo sapiens SRY (sex determining region Y)-box 5012 4 (SOX4), mRNA	5012	99%	0.0	99%	U E G S M
NM_003108.3	Homo sapiens SRY (sex determining region Y)-box 309 11 (SOX11), mRNA	440	13%	1e-80	86%	U E G S M
NM_006943.2	Homo sapiens SRY (sex determining region Y)-box 291 12 (SOX12), mRNA	422	12%	3e-75	88%	U E G S M
NM_006941.3	Homo sapiens SRY (sex determining region Y)-box 167 10 (SOX10), mRNA	167	7%	7e-38	77%	U E G S M
NM_000346.2	Homo sapiens SRY (sex determining region Y)-box 156 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA	156	7%	1e-34	75%	U E G S M
NM_007084.2	Homo sapiens SRY (sex determining region Y)-box 21 21 (SOX21), mRNA	140	7%	1e-29	74%	U E G S M
NM_006942.1	Homo sapiens SRY (sex determining region Y)-box 129 15 (SOX15), mRNA	129	7%	2e-26	74%	U E G S M
NM_014587.2	Homo sapiens SRY (sex determining region Y)-box 127 8 (SOX8), mRNA	127	8%	7e-26	71%	U E G S M
NM_031439.2	Homo sapiens SRY (sex determining region Y)-box 113 7 (SOX7), mRNA	113	7%	1e-21	71%	U E G S M
NM_018419.2	Homo sapiens SRY (sex determining region Y)-box 107 18 (SOX18), mRNA	107	7%	6e-20	71%	U E G S M
NM_004189.2	Homo sapiens SRY (sex determining region Y)-box 104 14 (SOX14), mRNA	104	7%	8e-19	71%	U E G S M
NM_022454.3	Homo sapiens SRY (sex determining region Y)-box 100 17 (SOX17), mRNA	100	7%	9e-18	71%	U E G S M
NM_005634.2	Homo sapiens SRY (sex determining region Y)-box 100 3 (SOX3), mRNA	100	7%	9e-18	71%	U E G S M
NM_005986.2	Homo sapiens SRY (sex determining region Y)-box 96.9 1 (SOX1), mRNA	96.9	7%	1e-16	70%	U E G S M
NM_003106.2	Homo sapiens SRY (sex determining region Y)-box 91.5 2 (SOX2), mRNA	91.5	7%	5e-15	69%	U E G S M
NM_005686.2	Homo sapiens SRY (sex determining region Y)-box 78.8 13 (SOX13), mRNA	78.8	7%	3e-11	70%	U E G S M
XM_001713691.1	PREDICTED: Homo sapiens hypothetical protein LOC100130809 (LOC100130809), mRNA	64.4	4%	7e-07	74%	U E G S M
NM_003140.1	Homo sapiens sex determining region Y (SRY), mRNA	64.4	4%	7e-07	74%	U E G S M
NM_152989.2	Homo sapiens SRY (sex determining region Y)-box 57.2 5 (SOX5), transcript variant 2, mRNA	57.2	3%	1e-04	73%	U E G S M
NM_006940.4	Homo sapiens SRY (sex determining region Y)-box 57.2 5 (SOX5), transcript variant 1, mRNA	57.2	3%	1e-04	73%	U E G S M
NM_178010.1	Homo sapiens SRY (sex determining region Y)-box 57.2 5 (SOX5), transcript variant 3, mRNA	57.2	3%	1e-04	73%	U E G S M
NM_052876.2	Homo sapiens BTB (POZ) domain containing 14B (BTBD14B), mRNA	51.8	1%	0.004	89%	U E G S M
NM_033326.2	Homo sapiens SRY (sex determining region Y)-box 50.0 6 (SOX6), transcript variant 2, mRNA	50.0	3%	0.014	72%	U E G S M
NM_017508.1	Homo sapiens SRY (sex determining region Y)-box 50.0 6 (SOX6), transcript variant 1, mRNA	50.0	3%	0.014	72%	U E G S M

XM_001132155.2	PREDICTED: Homo sapiens similar to Afadin (Protein AF-6) (LOC730031), mRNA	46.4	46.4	1%	0.18	88%	GM
NM_001040001.1	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 1, mRNA	46.4	46.4	1%	0.18	88%	UE GM
NM_001040000.1	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 2, mRNA	46.4	46.4	1%	0.18	88%	UE GM
NM_005936.2	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 (MLLT4), transcript variant 3, mRNA	46.4	46.4	1%	0.18	88%	UE GM
NM_015156.2	Homo sapiens REST corepressor 1 (RCOR1), mRNA	44.6	44.6	1%	0.62	83%	UE GM

Genomic sequences [show first]

NT_007592.14	Homo sapiens chromosome 6 genomic contig, reference assembly	5012	5094	99%	0.0	99%	
NW_001838973.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279188126)	1570	3057	60%	0.0	100%	
NW_001838765.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188139)	309	440	13%	1e-80	86%	
NT_005334.15	Homo sapiens chromosome 2 genomic contig, reference assembly	309	440	13%	1e-80	86%	
NW_001838652.1	Homo sapiens chromosome 20 genomic contig, alternate assembly (based on HuRef SCAF_1103279188366)	291	601	13%	3e-75	88%	
NT_011387.8	Homo sapiens chromosome 20 genomic contig, reference assembly	291	601	13%	3e-75	88%	
NW_001838084.2	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188152)	140	182	8%	1e-29	90%	
NT_009952.14	Homo sapiens chromosome 13 genomic contig, reference assembly	140	182	8%	1e-29	90%	
NW_001838403.1	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on HuRef SCAF_1103279188371)	129	129	7%	2e-26	74%	
NT_010718.15	Homo sapiens chromosome 17 genomic contig, reference assembly	129	129	7%	2e-26	74%	
NW_001838454.2	Homo sapiens chromosome 17 genomic contig, alternate assembly (based on HuRef SCAF_1103279188168)	104	246	8%	8e-19	90%	
NW_001838884.2	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on HuRef SCAF_1103279188385)	104	366	11%	8e-19	92%	
NT_010641.15	Homo sapiens chromosome 17 genomic contig, reference assembly	104	163	7%	8e-19	78%	
NT_005612.15	Homo sapiens chromosome 3 genomic contig, reference assembly	104	448	11%	8e-19	92%	
NW_001842405.1	Homo sapiens chromosome X genomic contig, alternate assembly (based on HuRef SCAF_1103279188404)	100	141	8%	9e-18	87%	
NT_011786.15	Homo sapiens chromosome X genomic contig, reference assembly	100	223	10%	9e-18	92%	
NT_027140.6	Homo sapiens chromosome 13 genomic contig, reference assembly	96.9	137	8%	1e-16	92%	
NW_001838745.1	Homo sapiens chromosome 22 genomic contig,	95.1	255	9%	4e-16	96%	

	alternate assembly (based on HuRef SCAF_1103279188372)					
NT_011520.11	Homo sapiens chromosome 22 genomic contig, reference assembly	95.1	255	9%	4e-16	96%
NW_001839122.2	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279188150)	87.8	141	6%	6e-14	87%
NT_077531.3	Homo sapiens chromosome 8 genomic contig, reference assembly	87.8	141	6%	6e-14	87%
NW_001838339.2	Homo sapiens chromosome 16 genomic contig, alternate assembly (based on HuRef SCAF_1103279188181)	86.0	139	7%	2e-13	77%
NT_037887.4	Homo sapiens chromosome 16 genomic contig, reference assembly	86.0	139	7%	2e-13	77%
NW_001838533.2	Homo sapiens chromosome 1 genomic contig, alternate assembly (based on HuRef SCAF_1103279188157)	77.0	335	6%	1e-10	100%
NW_001838085.1	Homo sapiens chromosome 13 genomic contig, alternate assembly (based on HuRef SCAF_1103279188104)	77.0	117	4%	1e-10	92%
NT_004487.18	Homo sapiens chromosome 1 genomic contig, reference assembly	77.0	376	6%	1e-10	100%
NW_001839132.1	Homo sapiens chromosome 8 genomic contig, alternate assembly (based on HuRef SCAF_1103279188282)	66.2	285	7%	2e-07	92%
NT_008183.18	Homo sapiens chromosome 8 genomic contig, reference assembly	66.2	328	7%	2e-07	92%
NW_001842422.1	Homo sapiens chromosome Y genomic contig, alternate assembly (based on HuRef SCAF_1103279188414)	64.4	108	5%	7e-07	84%
NT_011896.9	Homo sapiens chromosome Y genomic contig, reference assembly	64.4	192	7%	7e-07	87%
NT_011333.5	Homo sapiens chromosome 20 genomic contig, reference assembly	62.6	116	6%	2e-06	79%
NW_001838052.1	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on HuRef SCAF_1103279188408)	57.2	140	5%	1e-04	96%
NT_009714.16	Homo sapiens chromosome 12 genomic contig, reference assembly	57.2	181	5%	1e-04	96%
NW_001838671.1	Homo sapiens chromosome 20 genomic contig, alternate assembly (based on HuRef SCAF_1103279188118)	53.6	53.6	2%	0.001	79%
NW_001838954.2	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188298)	51.8	180	5%	0.004	90%
NT_011295.10	Homo sapiens chromosome 19 genomic contig, reference assembly	51.8	92.7	2%	0.004	96%
NT_023133.12	Homo sapiens chromosome 5 genomic contig, reference assembly	51.8	180	5%	0.004	90%
NW_001838022.2	Homo sapiens chromosome 11 genomic contig, alternate assembly (based on HuRef SCAF_1103279188392)	50.0	131	5%	0.014	92%
NW_001838468.1	Homo sapiens chromosome 18 genomic contig, alternate assembly (based on HuRef SCAF_1103279188038)	50.0	50.0	1%	0.014	87%
NW_001838951.1	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188395)	50.0	94.5	1%	0.014	87%
NW_001838865.2	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188138)	50.0	50.0	1%	0.014	87%

NT_006576.15	Homo sapiens chromosome 5 genomic contig, reference assembly	50.0	131	2%	0.014	100%
NT_009237.17	Homo sapiens chromosome 11 genomic contig, reference assembly	50.0	131	5%	0.014	92%
NT_007819.16	Homo sapiens chromosome 7 genomic contig, reference assembly	50.0	347	6%	0.014	96%
NT_010966.13	Homo sapiens chromosome 18 genomic contig, reference assembly	50.0	50.0	1%	0.014	87%
NT_010393.15	Homo sapiens chromosome 16 genomic contig, reference assembly	50.0	131	3%	0.014	92%
NT_005403.16	Homo sapiens chromosome 2 genomic contig, reference assembly	50.0	176	3%	0.014	100%
NT_006713.14	Homo sapiens chromosome 5 genomic contig, reference assembly	50.0	135	1%	0.014	88%
NW_001838061.2	Homo sapiens chromosome 12 genomic contig, alternate assembly (based on HuRef SCAF_1103279188362)	46.4	251	1%	0.18	92%
NW_001838006.2	Homo sapiens chromosome 10 genomic contig, alternate assembly (based on HuRef SCAF_1103279188397)	46.4	130	1%	0.18	93%
NW_001838988.2	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279187031)	46.4	46.4	1%	0.18	93%
NT_025741.14	Homo sapiens chromosome 6 genomic contig, reference assembly	46.4	210	3%	0.18	93%
NT_113898.1	Homo sapiens chromosome 6 genomic contig, reference assembly	46.4	46.4	1%	0.18	88%
NT_007302.13	Homo sapiens chromosome 6 genomic contig, reference assembly	46.4	46.4	1%	0.18	88%
NT_030059.12	Homo sapiens chromosome 10 genomic contig, reference assembly	46.4	171	1%	0.18	93%
NW_001838769.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188433)	44.6	210	4%	0.62	96%
NW_001838115.2	Homo sapiens chromosome 14 genomic contig, alternate assembly (based on HuRef SCAF_1103279188327)	44.6	85.5	2%	0.62	96%
NW_001838461.1	Homo sapiens chromosome 18 genomic contig, alternate assembly (based on HuRef SCAF_1103279188344)	44.6	44.6	1%	0.62	90%
NW_001838768.1	Homo sapiens chromosome 2 genomic contig, alternate assembly (based on HuRef SCAF_1103279188306)	44.6	44.6	1%	0.62	83%
NW_001838987.1	Homo sapiens chromosome 6 genomic contig, alternate assembly (based on HuRef SCAF_1103279188274B)	44.6	85.5	1%	0.62	92%
NW_001838928.2	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188369)	44.6	44.6	0%	0.62	96%
NW_001838915.1	Homo sapiens chromosome 4 genomic contig, alternate assembly (based on HuRef SCAF_1103279188399)	44.6	249	1%	0.62	96%
NW_001838878.1	Homo sapiens chromosome 3 genomic contig, alternate assembly (based on HuRef SCAF_1103279188187)	44.6	85.5	1%	0.62	90%
NW_001838953.2	Homo sapiens chromosome 5 genomic contig, alternate assembly (based on HuRef SCAF_1103279188146)	44.6	44.6	1%	0.62	88%
NT_026437.11	Homo sapiens chromosome 14 genomic contig, reference assembly	44.6	249	2%	0.62	92%
NT_016354.18		44.6	536	1%	0.62	96%

	Homo sapiens chromosome 4 genomic contig, reference assembly					
NT_023935.17	Homo sapiens chromosome 9 genomic contig, reference assembly	44.6	130	3%	0.62	92%
NT_008470.18	Homo sapiens chromosome 9 genomic contig, reference assembly	44.6	169	4%	0.62	93%
NT_022459.14	Homo sapiens chromosome 3 genomic contig, reference assembly	44.6	85.5	1%	0.62	90%
NT_032977.8	Homo sapiens chromosome 1 genomic contig, reference assembly	44.6	374	3%	0.62	96%
NT_010859.14	Homo sapiens chromosome 18 genomic contig, reference assembly	44.6	44.6	1%	0.62	90%

Alignments

>ref|NM_003107.2| **U E G M** Homo sapiens SRY (sex determining region Y)-box 4 (SOX4), mRNA
Length=4912

GENE ID: 6659 SOX4 | SRY (sex determining region Y)-box 4 [Homo sapiens]
(Over 10 PubMed links)

Score = 5012 bits (5558), Expect = 0.0
Identities = 2789/2793 (99%), Gaps = 2/2793 (0%)
Strand=Plus/Plus

Query	5	CCAGCATTGAGAAACTCCTCTCTACTTTAGCAGCGTCTCCAGACTCAGCCGAGAGACAG	64
Sbjct	449	CCAGCATTGAGAAACTCCTCTCTACTTTAGCAGCGTCTCCAGACTCAGCCGAGAGACAG	508
Query	65	CAAACCTGAGCGCGGTGAGAGAGCGAGAGAGAGGGAGAGAGACTCTCCAGCCTGGGAA	124
Sbjct	509	CAAACCTGAGCGCGGTGAGAGAGCGAGAGAGAGGGAGAGAGACTCTCCAGCCTGGGAA	568
Query	125	CTATAACTCCTCTGCGAGAGGCGGAGAACTCCTTCCCCAAATCTTTTGGGGACTTTTCTC	184
Sbjct	569	CTATAACTCCTCTGCGAGAGGCGGAGAACTCCTTCCCCAAATCTTTTGGGGACTTTTCTC	628
Query	185	TCTTTACCACTCCGCCCTGCGAGGAGTTGAGGGCCAGTTCGGCCGCCGCGCGCTC	244
Sbjct	629	TCTTTACCACTCCGCCCTGCGAGGAGTTGAGGGCCAGTTCGGCCGCCGCGCGCTC	688
Query	245	TTCCCGTTGCGGCTGTGCTTGGCCGGGGAACCGGAGGGCCCGGCGATCGCGGCGGC	304
Sbjct	689	TTCCCGTTGCGGCTGTGCTTGGCCGGGGAACCGGAGGGCCCGGCGATCGCGGCGGC	748
Query	305	CGCCGCGAGGGTGTGAGCGCGCTGGGCGCCCGGAGCCGAGGCGATGTCAGCAAAAC	364
Sbjct	749	CGCCGCGAGGGTGTGAGCGCGCTGGGCGCCCGGAGCCGAGGCGATGTCAGCAAAAC	808
Query	365	CAACAATGCCGAGAACACGGAAGCGCTGCTGGCCGGCGAGAGCTCGGACTCGGGCGCCG	424
Sbjct	809	CAACAATGCCGAGAACACGGAAGCGCTGCTGGCCGGCGAGAGCTCGGACTCGGGCGCCG	868
Query	425	CCTGAGCTGGGAATCGCCTCTCCCCACGCCCGGCTCCACGCCCTCCACGGGCGGCAA	484
Sbjct	869	CCTGAGCTGGGAATCGCCTCTCCCCACGCCCGGCTCCACGCCCTCCACGGGCGGCAA	928
Query	485	GGCCGACGACCCGAGCTGGTGAAGACCCCGAGTGGGACATCAAGCGACCCATGAACGC	544
Sbjct	929	GGCCGACGACCCGAGCTGGTGAAGACCCCGAGTGGGACATCAAGCGACCCATGAACGC	988
Query	545	CTTCATGGTGGTGCAGATCGAGCGGCGAAGATCATGGAGCAGTCGCCGACATGCA	604
Sbjct	989	CTTCATGGTGGTGCAGATCGAGCGGCGAAGATCATGGAGCAGTCGCCGACATGCA	1048
Query	605	CAACGCCGAGATCTCCAAGCGCTGGGCAAACTGCTGGAAGCTGCTCAAAGACAGCGACAA	664
Sbjct	1049	CAACGCCGAGATCTCCAAGCGCTGGGCAAACTGCTGGAAGCTGCTCAAAGACAGCGACAA	1108
Query	665	GATCCCTTTCAATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCGA	724
Sbjct	1109	GATCCCTTTCAATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCGA	1168
Query	725	CTACAAGTACCGGCCAGGAAGAAGTGAAGTCCGGCAACGCCAATCCAGCTCTCGGC	784
Sbjct	1169	CTACAAGTACCGGCCAGGAAGAAGTGAAGTCCGGCAACGCCAATCCAGCTCTCGGC	1228
Query	785	CGCCGCTCTCTCAAGCCGGGGGAGAGGGGAGACAGGTCAGTGGCGAGTGGCGGGGCGG	844
Sbjct	1229	CGCCGCTCTCTCAAGCCGGGGGAGAGGGGAGACAGGTCAGTGGCGAGTGGCGGGGCGG	1288
Query	845	CCATGGGGGCGGCGGCGGCGGGGAGCAGCAACGCGGGGGAGGAGGCGGCGGTGCGAG	904
Sbjct	1289	CCATGGGGGCGGCGGCGGCGGGGAGCAGCAACGCGGGGGAGGAGGCGGCGGTGCGAG	1348
Query	905	TGGCGGCGGCGCAACTCCAACCGGCGCAGAAAAAGAGCTGCGGCTCCAAGTGGCGGG	964
Sbjct	1349	TGGCGGCGGCGCAACTCCAACCGGCGCAGAAAAAGAGCTGCGGCTCCAAGTGGCGGG	1408

Query	965	CGGCGCGGGCGGTGGGGTTAGCAAACCCGACGCCAAGCTCATCTTGGCAgggggggggggg	1024
Sbjct	1409	CGGCGCGGGCGGTGGGGTTAGCAAACCCGACGCCAAGCTCATCTTGGCAGGCGGCGGG	1468
Query	1025	ggggggGAAAGCAGCGGCTgccccccgctcctctcggccgagcaacaggggggggggg	1084
Sbjct	1469	CGGCGGGAAGCAGCGGCTGCCGCCGCCCTCTTCGCCGCCGAACAGCGGGGGCGC	1528
Query	1085	ggcctctgctgccccctggggcgccggcgccgACCACCACTCGCTGTATCAAGGCGCGGACTTC	1144
Sbjct	1529	CGCCTGCTGTCGCCCTGGGCGCCGCCGCCGACCACCACTCGCTGTATCAAGGCGCGGACTTC	1588
Query	1145	CAGCGCCTCGGCCCTCCGCCCTCTCGGCAGCCTCGGCCCTCCGCAGCGCTCGCGGCCCGGG	1204
Sbjct	1589	CAGCGCCTCGGCCCTCCGCCCTCTCGGCAGCCTCGGCCCTCCGCAGCGCTCGCGGCCCGGG	1648
Query	1205	CAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCTACCTGTTTCGGCGGCCCTGGGCACGTC	1264
Sbjct	1649	CAAGCACCTGGCGGAGAAGAAGGTGAAGCGCGTCTACCTGTTTCGGCGGCCCTGGGCACGTC	1708
Query	1265	GTCGTGCCCTGTGGCGGCGTGGGCGGGGAGCCGACCCAGCGACCCCTGGGCTGTGA	1324
Sbjct	1709	GTCGTGCCCTGTGGCGGCGTGGGCGGGGAGCCGACCCAGCGACCCCTGGGCTGTGA	1768
Query	1325	CGAGGAGGAGGCGCGGGCTGCTggccggagcgccagcgccggcgagcgccggagcgcc	1384
Sbjct	1769	CGAGGAGGAGGCGCGGGCTGCTCGCCGACGCGGCCAGCCTGAGCGGCGCAGCAGCGC	1828
Query	1385	ggcctcgtccccccgcccggcgccggcgccggcgccgagccacggcggtacgccagcctgg	1444
Sbjct	1829	CGCCTCGTCCCCCGCGCGGCCGCTCGCCCGCGACACCGCGGCTACGCCAGCTGCG	1888
Query	1445	ggcgccctcggccggcccgctccagcgcgccgTCGCACGCGTccctctcggcgccgtccca	1504
Sbjct	1889	CGCGCCTCGGCCCGCCCGTCCAGCGCGCCTCGCAGCGGCTCCTCTCGGCCCTGCTCCA	1948
Query	1505	ctcctctctcttctcctcctcctgggctcctcgtcctccgagcgagaggttcgaagacGACCT	1564
Sbjct	1949	CTCTCTCTCTCTCTCTCTCGGCTCTCTCTCTCGCAGCAGAGTTCGAAGACGACCT	2008
Query	1565	GTCGACCTGAACCCAGCTCAAACTTTGAGAGCATGTCCTTGGGAGCTTCAGTTCGTC	1624
Sbjct	2009	GTCGACCTGAACCCAGCTCAAACTTTGAGAGCATGTCCTTGGGAGCTTCAGTTCGTC	2068
Query	1625	GTCGGCGCTCGACCGGGACCTGGATTTTAACTTCGAGCCCGGCTCCGGCTCGCACTTCGA	1684
Sbjct	2069	GTCGGCGCTCGACCGGGACCTGGATTTTAACTTCGAGCCCGGCTCCGGCTCGCACTTCGA	2128
Query	1685	GTTCGGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCGAGTC	1744
Sbjct	2129	GTTCGGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGAGACTGGCTCGAGTC	2188
Query	1745	CAGCATCTCCAACCTGGTTTTTACCCTACTGAAGGGCGCGCAGGCAGGGAGAAGGGCCaggg	1804
Sbjct	2189	CAGCATCTCCAACCTGGTTTTTACCCTACTGAAGGGCGCGCAGGCAGGGAGAAGGGCCGGG	2248
Query	1805	ggggggTAGGAGAGGAgaaaaaaaggtgaaaaaaagaaaaagcaaaagagagagaggt	1864
Sbjct	2249	GGGGGTAGGAGAGGAGAAAAAAGTGAAAAAAGAAACGAAAGGACAGACGAAGAGT	2308
Query	1865	tttaagagaaaggggaaagaaagaaagaaagaaaggttaagcagggCTCG-TTCGCCCGGTTCT	1923
Sbjct	2309	TTAAAGAGAAAAGGGAAAAAAGAAAGAAAAAGTAAGCAGGGCTGGCTTCGCCCGGTTCT	2368
Query	1924	CGTCGTCGGATCAAGGAGCGCGCGGCGCTTTTGACCCCGCGCTCCCATCCCCACCTTCC	1983
Sbjct	2369	CGTCGTCGGATCAAGGAGCGCGCGGCGCTTTTGACCCCGCGCTCCCATCCCCACCTTCC	2428
Query	1984	CGGGCCGGGGACCCACTCTGCCAGCCGAGGGACGCGGAGGAGAGAGGGTAGACAGG	2043
Sbjct	2429	CGGGCCGGGGACCCACTCTGCCAGCCGAGGGACGCGGAGGAGAGAGGGTAGACAGG	2488
Query	2044	GGCGACCTGTGATTGTTGTTATTGATGTTGTTGTTGATGGC-aaaaaaaagcGACATT	2102
Sbjct	2489	GGCGACCTGTGATTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAAAGGACATT	2548
Query	2103	CGAGTTTGCTCCCTTTTGCTTGAAGAGACCCCCCTCCCTTCCAACGAGCTTCGGGACTT	2162
Sbjct	2549	CGAGTTTGCTCCCTTTTGCTTGAAGAGACCCCCCTCCCTTCCAACGAGCTTCGGGACTT	2608
Query	2163	GCTGCACCCCGACGAAGAAGGCGAGTTAGTTTTCTAGAGACTTGAAGGAGTCTCCCCCT	2222

7/16/08

Strand=Plus/Plus

```

Query 1671 GGCTCGCACTTCGAGTTCCCGGACTACTGCACGCCCCGAGGTGAGCGAGATGATCTCGGGA 1730
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1277 GGCTCCCACTTCGAGTTCCCGGACTACTGCACGCCCCGAGGTGAGCGAGATGATCGCGGGG 1336
Query 1731 GACTGGCTCGAGTCCAGCATCTCAACCTGGTTTTCACCTACTGAAGGGCGC 1782
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1337 GACTGGCTGGAGGCGAACTTCTCCGACCTGGTGTTCACATATTGAAAGGGCGC 1388

```

>ref|NM_006943.2| **UEGM** Homo sapiens SRY (sex determining region Y)-box 12 (SOX12), mRNA
Length=4645

GENE ID: 6666 SOX12 | SRY (sex determining region Y)-box 12 [Homo sapiens]
(10 or fewer PubMed links)

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Score = 291 bits (322), Expect = 3e-75
Identities = 213/246 (86%), Gaps = 1/246 (0%)
Strand=Plus/Plus

```

Query 494 CCGAGCTGGTGAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCCTTCATGGT 553
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 418 CCGG-GCTGGTGAAGACCCCGAGCGGCCACATCAAGAGGCCGATGAACGCATTTCATGGT 476
Query 554 GTGGTCGAGATCGAGCGCGCAAGATCATGGAGCAGTCGCCCCGACATGCACAAACGCCGA 613
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 477 GTGGTCGAGCAGCAACGCGCGAAGATCATGGACCAGTGGCCCCGACATGCACAAACGCCGA 536
Query 614 GATCTCCAAGCGGCTGGGCAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTT 673
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 537 GATCTCCAAGCGCTGGGCGCGCGCTGGCAGCTGCTGCAGACTCGGAGAAGATCCCGTT 596
Query 674 CATTCGAGAGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTA 733
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 597 CGTGGGAGCGGAGCGGCTGCGGCTCAAGCACATGGCGGATTACCCGGACTACAAGTA 656
Query 734 CCGGCC 739
          |||||
Sbjct 657 CCGGCC 662

```

Score = 131 bits (144), Expect = 5e-27
Identities = 90/102 (88%), Gaps = 0/102 (0%)
Strand=Plus/Plus

```

Query 1674 TCGCACTTCGAGTTCCCGGACTACTGCACGCCCCGAGGTGAGCGAGATGATCTCGGGAGAC 1733
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1177 TCGCACTTCGAGTTCCCGGACTACTGCACCCCCGAGGTTACGAGATGATCGCGGGGAC 1236
Query 1734 TGGCTCGAGTCCAGCATCTCCAACCTGGTTTTCACCTACTGA 1775
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1237 TGGCGCCGCTAGCATCGCAGACCTGGTTTTCACCTACTGA 1278

```

>ref|NM_006941.3| **UEGM** Homo sapiens SRY (sex determining region Y)-box 10 (SOX10), mRNA
Length=2882

GENE ID: 6663 SOX10 | SRY (sex determining region Y)-box 10 [Homo sapiens]
(Over 10 PubMed links)

Score = 167 bits (184), Expect = 7e-38
Identities = 173/224 (77%), Gaps = 2/224 (0%)
Strand=Plus/Plus

```

Query 521 GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTTCGAGATCGAGCGGCAGAT 580
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 584 GCACGTCAAGCGGCCATGAACGCCTTCATGGTGTGGGCTCAGGCAGCGCGCAGGAAGCT 643
Query 581 CATGGAGCAGTCGCCCGACATGCACAAACGCCGAGATCTCAAAGCGGCTGGGCAACGCTG 640
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 644 CCGGACAGTACCCGACCTGCACAAACGCTGAGCTCAGCAAGACGCTGGGCAAGCTCTG 703
Query 641 GAAGCTGCTCAAAGACAGCGACAAGATCCCTTTTCATTGCA-GAGGCGGAGCGGCTGCGCC 699
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```



```

Sbjct 701 GCAGAACCCCAAGATGCACAACCTCCGAGATCTCCAAGCGCCTGGGCGCGCAGTGAAGCT 760
Query 647 GCTCAAGACGACGCGACAAGATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCA 706
Sbjct 761 GCTGGACGAGGACGAGAAGCGGCCCTTCGTGGAGGAGGCCAAGCGGCTCCGCGCCCGACA 820
Query 707 CATGGCTGACTACCCCGACTACAAGTACCGGCC 739
Sbjct 821 CCTGCGCGACTACCCCGACTACAAGTACCGGCC 853

```

>ref|NM_014587.2| **UEGM** Homo sapiens SRY (sex determining region Y)-box 8 (SOX8), mRNA
Length=3069

GENE ID: 30812 SOX8 | SRY (sex determining region Y)-box 8 [Homo sapiens]
(Over 10 PubMed links)

Score = 127 bits (140), Expect = 7e-26
Identities = 179/252 (71%), Gaps = 6/252 (2%)
Strand=Plus/Plus

```

Query 528 AAGCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGCGCAAGATCATGGAG 587
Sbjct 422 AAGCGGCCCATGAACGCATTTCATGGTGTGGGCGCAGGCGCGCGCCGAAGCTGGCCGAC 481
Query 588 CAGTCGCGCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAACGCTGGAAGCTG 647
Sbjct 482 CAGTACCGCGACCTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAAGCTGTGGCGCTTG 541
Query 648 CTCAAAGACAGCGACAAGATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCAC 707
Sbjct 542 CTGAGCGAGAGCGAGAAGCGGCCCTTCGTGGAGGAGGCGAGCGCCTTCGCGTGCAGCAC 601
Query 708 ATGGCTGACTACCCCGACTACAAGTAC-----CGGCCAGGAAGAAGGTGAAGTCCGGC 761
Sbjct 602 AAGAAGGACCACCCGACTACAAGTACAGCCACGGCGCAGGAAGAGCGCCAAGCGCGC 661
Query 762 AACGCCAACTCC 773
Sbjct 662 CACAGCGACTCC 673

```

>ref|NM_031439.2| **UEGM** Homo sapiens SRY (sex determining region Y)-box 7 (SOX7), mRNA
Length=3219

GENE ID: 83595 SOX7 | SRY (sex determining region Y)-box 7 [Homo sapiens]
(10 or fewer PubMed links)

Score = 113 bits (124), Expect = 1e-21
Identities = 159/223 (71%), Gaps = 3/223 (1%)
Strand=Plus/Plus

```

Query 530 GCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGCGCAAGATCATGGAGCA 589
Sbjct 217 GCGGCCCATGAACGCCTTCATGGTTTGGGCCAAGGACGAGAGGAAACGGCTGGCAGTGCA 276
Query 590 GTCGCGGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAACGCTGGAAGCTGCT 649
Sbjct 277 GAACCCGAGCTGCACAACGCCGAGCTCAGCAAGATGCTGGGAAAGTGTGGAAGGCGCT 336
Query 650 CAAAGACAGCGACAAGATCCCTTTTCATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACAT 709
Sbjct 337 GACGCTGTCCGAGAAGAGGCGGTACGTGGACGAGGCGGAGCGGCTGCGCCTGCAGCACAT 396
Query 710 GGCTGACTACCCCGACTACAAGTACCGGCC---CAGGAAGAAG 749
Sbjct 397 GCAGGACTACCCCAACTACAAGTACCGGCCGCGCAGGAAGAAG 439

```

>ref|NM_018419.2| **UEGM** Homo sapiens SRY (sex determining region Y)-box 18 (SOX18), mRNA
Length=1718

GENE ID: 54345 SOX18 | SRY (sex determining region Y)-box 18 [Homo sapiens]
(Over 10 PubMed links)

Score = 107 bits (118), Expect = 6e-20
Identities = 160/223 (71%), Gaps = 8/223 (3%)
Strand=Plus/Plus

7/16/08

```
Score = 100 bits (10), Expect = 9e-18
Identities = 154/216 (71%), Gaps = 8/216 (3%)
Strand=Plus/Plus

Query   528    AAGCGACCCATGAACGCCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT---CATG      584
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   418    AAACGGCCCATGAACGCCCTTCATGGTATGGTCCC CGGCGAGCGGCGCAAATATGCCCTG      477

Query   585    GAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAAACGTGGAAG      644
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   478    GAGAAC---CCCAAGATGCACAATTCTGAGATCAGCAAGCGCTTTGGGCGCCGACTGGAAA      534

Query   645    CTGCTCAAGACAGCGACAAAGATCCCTTTCAITCGA-GAGGCGGAGCGGCTGCGCCTCAA      703
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   535    CTGCTGACCAGCGCCGAGAAGCGACCAATTCAT-CGACGAGCCCAAGCGACTTCGGGCCGT      593

Query   704    GCACATGGCTGACTACCCGACTACAAGTACCGGCC       739
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct   594    GCACATGAAGGAGTATCCGGACTACAAGTACCGACC       629
```

```
>ref|NM_005986.2| U1EGM Homo sapiens SRY (sex determining region Y)-box 1 (SOX1), mRNA
Length=4108
```

GENE ID: 6656 SOX1 | SRY (sex determining region Y)-box 1 [Homo sapiens]
(10 or fewer PubMed links)

Score = 96.9 bits (106), Expect = 1e-16
Identities = 152/215 (70%), Gaps = 2/215 (0%)
Strand=Plus/Plus

Query	526	TCAAGCGACCCATGAACGCCCTTCATGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGG	585
Sbjct	212	TCAAACGGCCCATGAACGCCCTTCATGTGTGGTCCCGGGGACGCGGCGCAAGATGGCCC	271
Query	586	AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAACGCTGGAAGC	645
Sbjct	272	AGGAAGACCCCAAGATGCACAACCTCGAGATACGAACGCCTTGGGGCCGAGTGGAAGG	331
Query	646	TGCTCAAAGACAGCGCAAGATCCCTTTTCATTCTGA-GAGGCGGAGCGGCTGCGCTCAAG	704
Sbjct	332	TCATGTCCGAGGCTCGAAGAGCGGCCGTTCA-TCGACGAGGCGCAAGCGGCTGCGCGCGCTG	390
Query	705	CACATGGCTACTCCCGCATACAAGTACCGGCC	739
Sbjct	391	CACATGAAGGAGCACCCGGATTACAAGTACCGGCC	425

```
>ref|NM_003106.2| UEGM Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA
Length=2518
```

GENE ID: 6657 SOX2 | SRY (sex determining region Y)-box 2 [Homo sapiens]
(Over 10 PubMed links)

Score = 91.5 bits (100), Expect = 5e-15
Identities = 153/219 (69%), Gaps = 2/219 (0%)
Strand=Plus/Plus

Query	526	TCAAGCGCCCATGAACGCCCTTCATGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGG	585
Sbjct	549	TCAAGCGGCCCATGAATGCCCTTCATGTGTGGTCCCGGGCGAGCGGCGCAAGATGGCCC	608
Query	586	AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAACGCTGGAAGC	645
Sbjct	609	AGGAGAACCCCAAGATGCACAACCTCGAGATACGACAAGCGCTTGGCGCCGAGTGGA AAC	668
Query	646	TGCTCA AAGACAGCGCAAGATCCCTTTCATTGCA -GAGCGGAGCGGCTGCGCCTCAAG	704
Sbjct	669	TTTTGTCTGGAGACGGGAGAGCGGCCGCTTCA -TCGACAGCGCTAAGCGGCTGCGAGCGCTG	727
Query	705	CACATGGCTGACTACCCCGCATCAAGTACCGGGCCAGG	743
Sbjct	728	CACATGAAGGAGCACCCGGATTATAAATACCGGCCCGG	766

```
>ref|NM_005686.2| UEGM Homo sapiens SRY (sex determining region Y)-box 13 (SOX13), mRNA
Length=4088
```

GENE ID: 9580 SOX13 | SRY (sex determining region Y)-box 13 [Homo sapiens]

(Over 10 PubMed links)

Score = 78.8 bits (86), Expect = 3e-11
 Identities = 153/218 (70%), Gaps = 10/218 (4%)
 Strand=Plus/Plus

```

Query 522 CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGGCCGAAGATC 581
Sbjct 1862 CACATCAAGAGGCCCATGAACGCCTTCATGGTGTGGGCCAAGGATGAGCGGAGGAAGATC 1921

Query 582 ATG-GAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTG 640
Sbjct 1922 CTGCAAGCCTTC-CCAGACATGCACAACCTCCAGCATCAGCAAGATCCTTGGATCTCGCTG 1980

Query 641 GAAG---CTGCTCAAAGACAGCGACAAG-ATCCCTTTTCATTGAGAGCGCGGAGCGGCTGC 696
Sbjct 1981 GAAATCCATGACCAA--CCAG-GAGAAGCAGCCCTACTATGAG-GAACAGCGCGGCTGA 2036

Query 697 GCCTCAAGCACATGGGTGACTACCCCGACTACAAGTAC 734
Sbjct 2037 GCCGGCAGCACCCTGGAGAAGTATCTGACTACAAGTAC 2074
  
```

>ref|XM_001713691.1| **GM** PREDICTED: Homo sapiens hypothetical protein LOC100130809 (LOC10013 mRNA)
 Length=897

Score = 64.4 bits (70), Expect = 7e-07
 Identities = 94/126 (74%), Gaps = 8/126 (6%)
 Strand=Plus/Plus

```

Query 528 AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCGAGCGGCCGAAGAT---CAT 583
Sbjct 329 AAGCGACCCATGAACGCATTTCATCGTGTGGTCTCGCGATC-AGAGGCGCAAGATGGCTCT 387

Query 584 GGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAA 643
Sbjct 388 AGAG-AATC-CCAGA-ATGCGAAACTCAGAGATCAGCAAGCAGCTGGGATACCAAGTGGAA 444

Query 644 GCTGCT 649
Sbjct 445 AATGCT 450
  
```

>ref|NM_003140.1| **UEGM** Homo sapiens sex determining region Y (SRY), mRNA
 Length=897

GENE ID: 6736 SRY | sex determining region Y [Homo sapiens]
 (Over 10 PubMed links)

Score = 64.4 bits (70), Expect = 7e-07
 Identities = 94/126 (74%), Gaps = 8/126 (6%)
 Strand=Plus/Plus

```

Query 528 AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCGAGCGGCCGAAGAT---CAT 583
Sbjct 329 AAGCGACCCATGAACGCATTTCATCGTGTGGTCTCGCGATC-AGAGGCGCAAGATGGCTCT 387

Query 584 GGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAACGCTGGAA 643
Sbjct 388 AGAG-AATC-CCAGA-ATGCGAAACTCAGAGATCAGCAAGCAGCTGGGATACCAAGTGGAA 444

Query 644 GCTGCT 649
Sbjct 445 AATGCT 450
  
```

>ref|NM_152989.2| **UEGM** Homo sapiens SRY (sex determining region Y)-box 5 (SOX5), transcribed variant 2, mRNA
 Length=4563

GENE ID: 6660 SOX5 | SRY (sex determining region Y)-box 5 [Homo sapiens]
 (Over 10 PubMed links)

Score = 57.2 bits (62), Expect = 1e-04
 Identities = 76/103 (73%), Gaps = 2/103 (1%)
 Strand=Plus/Plus

Query	5	CCAGATTTCGAGAAACTCCTCTCTACTTTAGCAGCGTCTCCAGACTCAGCCGAGAGACAG	64
Sbjct	12452671	CCAGCATTTCGAGAAACTCCTCTCTACTTTAGCAGCGTCTCCAGACTCAGCCGAGAGACAG	12452730
Query	65	CAAACTGCGGGCGTGGAGAGAGCGAGAGAGAGGGAGAGAGAGACTCTCCAGCCTGGGAA	124
Sbjct	12452731	CAAACTGCAGCGCGGTGAGAGAGCGAGAGAGAGGGAGAGAGAGACTCTCCAGCCTGGGAA	12452790
Query	125	CTATAACTCCTCTGCGAGAGCGGAGAACTCCTTCCCCAAATCTTTTGGGGACTTTTCTC	184
Sbjct	12452791	CTATAACTCCTCTGCGAGAGCGGAGAACTCCTTCCCCAAATCTTTTGGGGACTTTTCTC	12452850
Query	185	TCITTTACCCACCTCCGCCCTTGCAGGAGTGTAGAGGGCCAGTTCGGCCGCCGCGCGGTC	244
Sbjct	12452851	TCITTTACCCACCTCCGCCCTTGCAGGAGTGTAGAGGGCCAGTTCGGCCGCCGCGCGGTC	12452910
Query	245	TTCCCGTTTCGGCGTGTGCTTGGCCCGGGGAACCGGAGGGGCCCGGCATCGCGCGCGGC	304
Sbjct	12452911	TTCCCGTTTCGGCGTGTGCTTGGCCCGGGGAACCGGAGGGGCCCGGCATCGCGCGCGGC	12452970
Query	305	CGCCGCGAGGGTGTGAGCGCGCGTGGCGCCCCGCCGAGCCGAGGCCATGGTCAGCAAAAC	364
Sbjct	12452971	CGCCCGGAGGGTGTGAGCGCGCGTGGCGCCCCGCCGAGCCGAGGCCATGGTCAGCAAAAC	12453030
Query	365	CAACAATCGCGAGAAACCGGAAGCGCTGCTGGCCGCGAGAGCTCGACTCGGGCGCCGG	424
Sbjct	12453031	CAACAATCGCGAGAAACCGGAAGCGCTGCTGGCCGCGAGAGCTCGACTCGGGCGCCGG	12453090
Query	425	CCTCGAGCTGGGAAATCGCTCTCTCCCCACGCCCGGCTCCACGCTCCACGGGCGGCAA	484
Sbjct	12453091	CCTCGAGCTGGGAAATCGCTCTCTCCCCACGCCCGGCTCCACGCTCCACGGGCGGCAA	12453150
Query	485	GGCCGACGACCCGAGCTGTGTGAAGACCCCGAGTGGGCACATCAAGCGACCATGAACGC	544

Sbjct	12453151	GGCCGACGACCCGAGCTGGTGCAGAACCCCGAGTGGGACATCAAGCGACCCATGAACGC	12453210
Query	545	CTTCATGGTGTGGTGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCGACATGCA	604
Sbjct	12453211	CTTCATGGTGTGGTGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCGACATGCA	12453270
Query	605	CAACGCCGAGATCTCCAAGCGGCTGGGCAAAACGCTGGAAGCTGCTCAAAGACAGCGACAA	664
Sbjct	12453271	CAACGCCGAGATCTCCAAGCGGCTGGGCAAAACGCTGGAAGCTGCTCAAAGACAGCGACAA	12453330
Query	665	GATCCCTTTCAITTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCGA	724
Sbjct	12453331	GATCCCTTTCAITTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCGA	12453390
Query	725	CTACAAGTACCGGCCAGGAAGAAGTGAAGTCCGGCAACGCCAACATCCAGCTCCTCGGC	784
Sbjct	12453391	CTACAAGTACCGGCCAGGAAGAAGTGAAGTCCGGCAACGCCAACATCCAGCTCCTCGGC	12453450
Query	785	CGCCGCTCCTCCAAAGCCGGGGAGAGAGGAGACAAGTGTGGCGAGTGGCGGGGGCGG	844
Sbjct	12453451	CGCCGCTCCTCCAAAGCCGGGGAGAGAGGAGACAAGTGTGGCGAGTGGCGGGGGCGG	12453510
Query	845	ccatggggggcgggcgggcgggcgggagcagcaacgagggggagggcgagggcgagggcgag	904
Sbjct	12453511	CCATGGGGCGGCGCGCGGCGGGAGCAGCAACCGGGGGGAGGAGCGCGGCTGCGAG	12453570
Query	905	ggggcgggcgggcCAACTCCAAACCGGCGCAGAAAAAGAGCTCGCGCTCCAAAGTGGCGGG	964
Sbjct	12453571	TGGCGCGCGCGCCAACCTCAAACCGGCGCAGAAAAAGAGCTCGCGCTCCAAAGTGGCGGG	12453630
Query	965	CGGCGCGGCGGTGGGGTTAGCAAAACCGCACGCCAAGCTCATCTTGCGACggggcgggcggg	1024
Sbjct	12453631	CGGCGCGGCGGTGGGGTTAGCAAAACCGCACGCCAAGCTCATCTTGCGAGCGCGGCGG	12453690
Query	1025	cgggcggaagagcagcggtgcggcgcgcggtctctctggcgcgcggaacggcgggggcgcg	1084
Sbjct	12453691	CGCGGGGAAGAGCAGCGCTGCGCGCGCGCGCTCCTTCGCGCGCGAACAGCGGGGGCGCG	12453750
Query	1085	cgccctgctgcccctggggcgcgcgcgacacacactcgctgtacaaggcgcgactcc	1144
Sbjct	12453751	CGCCCTGCTGCCCTTGGGCGCGCGCGCGGACACACACTCGCTGTACAAGCGCGGACTCC	12453810
Query	1145	CAGCGCCTCGGCCTCCGCCTCCTTCGGCAGCCTCGGCCTCCGCAGCGCTCGCGGCCCGGG	1204
Sbjct	12453811	CAGCGCCTCGGCCTCCGCCTCCTTCGGCAGCCTCGGCCTCCGCAGCGCTCGCGGCCCGGG	12453870
Query	1205	CAAGCACCTGGCGGAGAAGAAGTGAAGCGCGTCTACTGTTTCGGCGGCTTGGGCACGTC	1264
Sbjct	12453871	CAAGCACCTGGCGGAGAAGAAGTGAAGCGCGTCTACTGTTTCGGCGGCTTGGGCACGTC	12453930
Query	1265	GTCGTGCCCCGTGGGCGGCGTGGGCGGGGAGCCGACCCAGCGACCCCTTGGGCTGTGA	1324
Sbjct	12453931	GTCGTGCCCCGTGGGCGGCGTGGGCGGGGAGCCGACCCAGCGACCCCTTGGGCTGTGA	12453990
Query	1325	CGAGGAGGAGGGCGCGGGCTGCTcgccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	1384
Sbjct	12453991	CGAGGAGGAGGGCGCGGGCTGCTCGCCGACGCGCCAGCGCTAGCGGCGCAGCAGCGC	12454050
Query	1385	cgccctcgcccccgcgcgggcg	1444
Sbjct	12454051	CGCCTCGTCCCCCGCGCGGCGCTCGCGCGCGACACCGCGGCTACGCGAGCTCGG	12454110
Query	1445	cgccgcctcgcccccg	1504
Sbjct	12454111	CGCGCCTCGCCGCGCCGCTCCAGCGCGCCTTCGACAGCGTCTCTCTCGGCTCTGCCA	12454170
Query	1505	ct	1564
Sbjct	12454171	CT	12454230
Query	1565	GCTCGACCTGAACCCAGCTCAAACCTTTGAGAGCATGTCCTTGGGACGTTTCAGTTCGTC	1624
Sbjct	12454231	GCTCGACCTGAACCCAGCTCAAACCTTTGAGAGCATGTCCTTGGGACGTTTCAGTTCGTC	12454290
Query	1625	GTCGGCGCTCGACCGGACCTGGATTTAACTTCGAGCCCGGCTTCGGCTCGCACTTCGA	1684
Sbjct	12454291	GTCGGCGCTCGACCGGACCTGGATTTAACTTCGAGCCCGGCTTCGGCTCGCACTTCGA	12454350
Query	1685	GTTCGCGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGAGAGCTTGGCTCGAGTC	1744
Sbjct	12454351	GTTCGCGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGAGAGCTTGGCTCGAGTC	12454410

Query	1745	CAGCATCTCCAACTCGTGTTCCTACTGGAAGGGCGCGCAGGCAGGGAGAAGGGCCGGG	1804
Sbjct	12454411	CAGCATCTCCAACTCGTGTTCCTACTGGAAGGGCGCGCAGGCAGGGAGAAGGGCCGGG	12454470
Query	1805	gggggTAGGAGAGGAgaaaaaaaaggggtaaaaaaaagggggaagggagagagagag	1864
Sbjct	12454471	GGGGGTAGGAGAGGAGAAAAAAAAGTGAATAAAAGAAACGAAAGGACAGACGAAGAGT	12454530
Query	1865	tttaaaagggggaagggggaagggggaagggggaagggggaagggggaagggggaagggg	1923
Sbjct	12454531	TTAAAGAGAAAAAGGAAAAAAGAAAGAAAAAGTAAGCAGGGCTGGCTTCGCCCGCTTCT	12454590
Query	1924	CGTCGTGGATCAAGAGAGCGGGCGGCGTTCCTGACCCGCGCTCCATCCCCACCTTC	1983
Sbjct	12454591	CGTCGTGGATCAAGAGAGCGGGCGGCGTTCCTGACCCGCGCTCCATCCCCACCTTC	12454650
Query	1984	CGGGCCGGGGACCCACTCTGCCAGCCGAGGGACGCGAGGAGGAAGAGGGTAGACAGG	2043
Sbjct	12454651	CGGGCCGGGGACCCACTCTGCCAGCCGAGGGACGCGAGGAGGAAGAGGGTAGACAGG	12454710
Query	2044	GGCGACCTGTGATTGTGTTTATGATGTTGTTGTTGATGTC-aaaaaaaggggagagag	2102
Sbjct	12454711	GGCGACCTGTGATTGTGTTTATGATGTTGTTGTTGATGTCAGAAAAAAGAGGCGACTT	12454770
Query	2103	CGAGTTTGCTCCCTTTGCTTGAAGAGACCCCTCCCTTCCACAGAGCTTCCGGACTT	2162
Sbjct	12454771	CGAGTTTGCTCCCTTTGCTTGAAGAGACCCCTCCCTTCCACAGAGCTTCCGGACTT	12454830
Query	2163	GTCGACCCCCAGCAAGAAGGCGAGTTAGTTTCTAGAGACTTGAAGAGTCTCCCCCT	2222
Sbjct	12454831	GTCGACCCCCAGCAAGAAGGCGAGTTAGTTTCTAGAGACTTGAAGAGTCTCCCCCT	12454890
Query	2223	TCCTGCATCACCACCTTGGTTTTGTTTTATTTTGGCTCTCTGGTCAAGAAAGAGGGGAGA	2282
Sbjct	12454891	TCCGTCATCACCACCTTGGTTTTGTTTTATTTTGGCTCTCTGGTCAAGAAAGAGGGGAGA	12454950
Query	2283	ACCCAGCGCACCCCTCCCGCTTTTAAACGCGTGATGAAGACAGAAGGCTCCGGGG	2342
Sbjct	12454951	ACCCAGCGCACCCCTCCCGCTTTTAAACGCGTGATGAAGACAGAAGGCTCCGGGG	12455010
Query	2343	TGACGAATTTGGCGCATGGCAGATGTTTGGGGGAACGCCGGGACTGAGAGACTCCACGC	2402
Sbjct	12455011	TGACGAATTTGGCGCATGGCAGATGTTTGGGGGAACGCCGGGACTGAGAGACTCCACGC	12455070
Query	2403	AGGCGAATTCCTGTTGGGGGCTTTTTTCTCCCTCTTTTCCCTTCCCGCTCTGCAG	2462
Sbjct	12455071	AGGCGAATTCCTGTTGGGGGCTTTTTTCTCCCTCTTTTCCCTTCCCGCTCTGCAG	12455130
Query	2463	CCGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGACCGGCGCTAGGAAATGAC	2522
Sbjct	12455131	CCGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGACCGGCGCTAGGAAATGAC	12455190
Query	2523	CCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGGCGGGGGCGGAGGAGACACG	2582
Sbjct	12455191	CCGAGAACCCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGGCGGGGGCGGAGGAGACACG	12455250
Query	2583	AACCTGAAGGGGGTTACGGTCAAACTGAAATGGATTGACAGTGGGGAGCTGGCGGGG	2642
Sbjct	12455251	AACCTGAAGGGGGTTACGGTCAAACTGAAATGGATTGACAGTGGGGAGCTGGCGGGG	12455310
Query	2643	GCGGCTGCTGGGCCCTCCGCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCAGA	2702
Sbjct	12455311	GCGGCTGCTGGGCCCTCCGCTTCTTTTCTACGTGAAATCAGTGAGGTGAGACTTCCAGA	12455370
Query	2703	CCCCGAGGCGTGAGGAGAGAGAGACTGTTTATGATGTTGACAGGGGCGAGTCAGTGGAGG	2762
Sbjct	12455371	CCCCGAGGCGTGAGGAGAGAGAGACTGTTTATGATGTTGACAGGGGCGAGTCAGTGGAGG	12455430
Query	2763	CGAGTGGTTTCGGGgaaaaaaaagggggaagggggaagggggaagggggaagggggaagggg	2795
Sbjct	12455431	CGAGTGGTTTCGGGAAAAAAGAAAAAAG 12455463	

Features in this part of subject sequence:

butyrophilin, subfamily 2, member A1 isoform 1 precursor
 butyrophilin, subfamily 2, member A1 isoform 2 precursor

Score = 41.0 bits (44), Expect = 7.5
 Identities = 30/35 (85%), Gaps = 0/35 (0%)
 Strand=Plus/Plus

Query 2048 ACCTGTGATTGTTGTTATTGATGTTGTTGTTGATG 2082

Query	725	CTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCCAGCTCCTCGGC	784
Sbjct	17883984	CTACAAGTACCGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCCAGCTCCTCGGC	17884043
Query	785	CGCGCCCTCTTCCAAGCCGGGGGAGAGGAGACAAAGTCGGTGGCAGTGGCGGGGGCGG	844
Sbjct	17884044	CGCGCCCTCTTCCAAGCCGGGGGAGAGGAGACAAAGTCGGTGGCAGTGGCGGGGGCGG	17884103
Query	845	CCATGGGGGCGGCGGCGGCGGGAGCAG	874
Sbjct	17884104	CCATGGGGGCGGCGGCGGCGGGAGCAG	17884133

Features in this part of subject sequence:

SRY (sex determining region Y)-box 4

Score = 1487 bits (1648), Expect = 0.0
 Identities = 829/831 (99%), Gaps = 1/831 (0%)
 Strand=Plus/Plus

Query	1966	TCCCATCCCCACCTTCCCGGGCGGGGACCCACTCTGCCAGCCGGAGGACGCGGAGG	2025
Sbjct	17884827	TCCCATCCCCACCTTCCCGGGCGGGGACCCACTCTGCCAGCCGGAGGACGCGGAGG	17884886
Query	2026	AGGAAGAGGGGTAGACAGGGGCGACCTGTGATTGTTGTTATGATGTTGTTGTTGATGGC	2085
Sbjct	17884887	AGGAAGAGGGGTAGACAGGGGCGACCTGTGATTGTTGTTATGATGTTGTTGTTGATGGCA	17884946
Query	2086	GGGAGAGGGGTAGACAGGGGCGACCTGTGATTGTTGTTATGATGTTGTTGTTGATGGCA	2144
Sbjct	17884947	GGGAGAGGGGTAGACAGGGGCGACCTGTGATTGTTGTTATGATGTTGTTGTTGATGGCA	17885006
Query	2145	CAACGAGCTTCCGGACTTGTCTGCACCCCGAGCAAGAAGGCGAGTTAGTTTCTAGAGAC	2204
Sbjct	17885007	CAACGAGCTTCCGGACTTGTCTGCACCCCGAGCAAGAAGGCGAGTTAGTTTCTAGAGAC	17885066
Query	2205	TTGAAGGAGTCTCCCCCTTCTGATCACCACCTTGGTTTGTGTTTATTTGCTTCTTGG	2264
Sbjct	17885067	TTGAAGGAGTCTCCCCCTTCTGATCACCACCTTGGTTTGTGTTTATTTGCTTCTTGG	17885126
Query	2265	TCAAGAAAGGAGGGGAGAACCCAGCGCACCCCTTCCCGGCTTTTAAACGCGTGATGA	2324
Sbjct	17885127	TCAAGAAAGGAGGGGAGAACCCAGCGCACCCCTTCCCGGCTTTTAAACGCGTGATGA	17885186
Query	2325	AGACAGAAGGCTCCGGGGTGACGAATTGGCCGATGGCAGATGTTTTGGGGGAACGCCGG	2384
Sbjct	17885187	AGACAGAAGGCTCCGGGGTGACGAATTGGCCGATGGCAGATGTTTTGGGGGAACGCCGG	17885246
Query	2385	GACTGAGAGACTCCACGCGAGCGAATTCCTGTTGGGGCCCTCTCTCTCTCTCTCTCTCT	2444
Sbjct	17885247	GACTGAGAGACTCCACGCGAGCGAATTCCTGTTGGGGCCCTCTCTCTCTCTCTCTCTCT	17885306
Query	2445	CCCTTGGCCCTCTCTGACCCGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGA	2504
Sbjct	17885307	CCCTTGGCCCTCTCTGACCCGAGGAGGAGATGTTGAGGGGAGGAGGCCAGCCAGTGTGA	17885366
Query	2505	CGGGCGCTAGGAAATGACCCGAGAACCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGGGG	2564
Sbjct	17885367	CGGGCGCTAGGAAATGACCCGAGAACCCGTTGGAAGCGCAGCAGCGGGAGCTAGGGGGG	17885426
Query	2565	GGGGCGGAGGAGGACAGAACTGGAAGGGGGTTACCGTCAAACGTAAATGGATTGTCAC	2624
Sbjct	17885427	GGGGCGGAGGAGGACAGAACTGGAAGGGGGTTACCGTCAAACGTAAATGGATTGTCAC	17885486
Query	2625	GTTGGGGAGCTGGCGCGCGGCTGCTGGGCTCCGCCCTCTTTTCTACGTGAAATCAGT	2684
Sbjct	17885487	GTTGGGGAGCTGGCGCGCGGCTGCTGGGCTCCGCCCTCTTTTCTACGTGAAATCAGT	17885546
Query	2685	GAGGTGAGACTTCCAGACCCCGAGGCGTGGAGGAGAGGAGACTGTTGATGTGGTACA	2744
Sbjct	17885547	GAGGTGAGACTTCCAGACCCCGAGGCGTGGAGGAGAGGAGACTGTTGATGTGGTACA	17885606
Query	2745	GGGGCAGTCAGTGGAGGGCGAGTGGTTTCGGGAGAGAGAGAGAGAGAGAGAGAGAGAG	2795
Sbjct	17885607	GGGGCAGTCAGTGGAGGGCGAGTGGTTTCGGGAGAGAGAGAGAGAGAGAGAGAGAGAG	17885657

>ref|NW_001838765.1|Hs2_WGA158_36 Homo sapiens chromosome 2 genomic contig, alternate asse
 (based on HuRef SCAF_1103279188139)
 Length=2797789

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features in this part of subject sequence:

SRY-box 11

Score = 309 bits (342), Expect = 1e-80
 Identities = 224/259 (86%), Gaps = 0/259 (0%)
 Strand=Plus/Plus


Query	491	CGACCCGAGCTGGTGCAGACCCCGAGTGGGCACATCAAGCGACCATGAACGCCITTCAT	550
Sbjct	719581	CGACCCGAGCTGGTGCAGACCGGCGTCGGGCCACATCAAGCGGCCGATGAACGCGTTCAT	719640
Query	551	GGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCGACATGCACAACGC	610
Sbjct	719641	GGTATGGTCCAAGATCGAACGAGGAAGATCATGGAGCAGTCTCCGGACATGCACAACGC	719700
Query	611	CGAGATCTCCAAGCGGCTGGGCAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCC	670
Sbjct	719701	CGAGATCTCCAAGAGGCTGGGCAAGCGCTGGAATAATGCTGAAGGACAGCGAGAAGATCCC	719760
Query	671	TTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCAGATGGCTGACTACCCCGACTACAA	730
Sbjct	719761	GTTTCATCCGGGAGGCGGAGCGGCTGCGGCTCAAGCAGATGGCGACTACCCCGACTACAA	719820
Query	731	GTACCGGCCAGGAAGAAG	749
Sbjct	719821	GTACCGGCCCGGAAAAAG	719839

Features in this part of subject sequence:

SRY-box 11

Score = 131 bits (144), Expect = 5e-27
 Identities = 96/112 (85%), Gaps = 0/112 (0%)
 Strand=Plus/Plus

Query	1671	GGCTCGCACTTCGAGITCCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCTCGGGA	1730
Sbjct	720692	GGCTCCCACTTCGAGITCCCGGACTACTGCACGCCGAGGTGAGCGAGATGATCGCGGGG	720751
Query	1731	GACTGGCTCGAGTCCAGCATCTCCAACCTGGTITTCACCTACTGAAGGGCGC	1782
Sbjct	720752	GACTGGCTGGAGGCGAATCTCTCGACCTGGTGTTCACATATTGAAGGGCGC	720803

>ref|NT_005334.15|Hs2_5491  Homo sapiens chromosome 2 genomic contig, reference assembly
 Length=11088087

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features in this part of subject sequence:

SRY-box 11

Score = 309 bits (342), Expect = 1e-80
 Identities = 224/259 (86%), Gaps = 0/259 (0%)
 Strand=Plus/Plus

Query	491	CGACCCGAGCTGGTGCAGACCCCGAGTGGGCACATCAAGCGACCATGAACGCCITTCAT	550
Sbjct	667099	CGACCCGAGCTGGTGCAGACCGGCGTCGGGCCACATCAAGCGGCCGATGAACGCGTTCAT	667158
Query	551	GGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCGACATGCACAACGC	610
Sbjct	667159	GGTATGGTCCAAGATCGAACGAGGAAGATCATGGAGCAGTCTCCGGACATGCACAACGC	667218
Query	611	CGAGATCTCCAAGCGGCTGGGCAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCC	670
Sbjct	667219	CGAGATCTCCAAGAGGCTGGGCAAGCGCTGGAATAATGCTGAAGGACAGCGAGAAGATCCC	667278
Query	671	TTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCAGATGGCTGACTACCCCGACTACAA	730
Sbjct	667279	GTTTCATCCGGGAGGCGGAGCGGCTGCGGCTCAAGCAGATGGCGACTACCCCGACTACAA	667338
Query	731	GTACCGGCCAGGAAGAAG	749

Sbjct 667339 GTACCGGCCCGGAAAAAG 667357

Features in this part of subject sequence:
SRY-box 11

Score = 131 bits (144), Expect = 5e-27
Identities = 96/112 (85%), Gaps = 0/112 (0%)
Strand=Plus/Plus

Query 1671 GGCTCGCACTTCGAGTTCGCCGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGA 1730
Sbjct 668210 GGCTCCCACTTCGAGTTCGCCGACTACTGCACGCCCGAGGTGAGCGAGATGATCGCGGGG 668269
Query 1731 GACTGGCTCGAGTCCAGCATCTCCAACCTGGTITTCACCTACTGAAGGGCGC 1782
Sbjct 668270 GACTGGCTGGAGGCGAAGTTCCTCCGACCTGGTGTTCACATATTGAAAGGGCGC 668321

>ref|NW_001838652.1|Hs20_WGA1211_36 Homo sapiens chromosome 20 genomic contig, alternate a
(based on HuRef SCAF_1103279188366)
Length=22415471

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY (sex determining region Y)-box 12

Score = 291 bits (322), Expect = 3e-75
Identities = 213/246 (86%), Gaps = 1/246 (0%)
Strand=Plus/Plus

Query 494 CCGGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCCATGAACGCCCTTCATGGT 553
Sbjct 258081 CCGG-GCTGGTGCAAGACCCCGAGCGGCCACATCAAGAGGCCGATGAACGCCATTTCATGGT 258139
Query 554 GTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCCGACATGCACAACGCCGA 613
Sbjct 258140 GTGGTCGCAGCAGCAACGGCGGAAGATCATGGAGCAGTGGCCCGACATGCACAACGCCGA 258199
Query 614 GATCTCCAAGCGGCTGGGCAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTT 673
Sbjct 258200 GATCTCCAAGCGGCTGGGCGCGGCTGGCAGCTGCTGCAGACTCGGAGAAGATCCCGTT 258259
Query 674 CATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTA 733
Sbjct 258260 CGTGGCGGAGGCGGAGCGGCTGCGGCTCAAGCACATGGCGGATTACCCGGACTACAAGTA 258319
Query 734 CCGGCC 739
Sbjct 258320 CCGGCC 258325

Features in this part of subject sequence:
SRY (sex determining region Y)-box 12

Score = 131 bits (144), Expect = 5e-27
Identities = 90/102 (88%), Gaps = 0/102 (0%)
Strand=Plus/Plus

Query 1674 TCGCACTTCGAGTTCGCCGACTACTGCACGCCCGAGGTGAGCGAGATGATCTCGGGAGAC 1733
Sbjct 258840 TCGCACTTCGAGTTCGCCGACTACTGCACGCCCGAGGTACCGAGATGATCGCGGGGGAC 258899
Query 1734 TGGCTCGAGTCCAGCATCTCCAACCTGGTITTCACCTACTGA 1775
Sbjct 258900 TGGCGCCGCTAGCATCGCAGACCTGGTITTCACCTACTGA 258941

Features in this part of subject sequence:
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62
Identities = 33/39 (84%), Gaps = 0/39 (0%)
Strand=Plus/Minus

```

Query    1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC    1186
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct    9967415    CGCCTCGGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC    9967377

```

Features in this part of subject sequence:
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62
Identities = 33/39 (84%), Gaps = 0/39 (0%)
Strand=Plus/Minus

```

Query    1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC    1186
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct    9967421    CGCCTCGGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC    9967383

```

Features in this part of subject sequence:
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62
Identities = 33/39 (84%), Gaps = 0/39 (0%)
Strand=Plus/Minus

```

Query    1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC    1186
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct    9967427    CGCCTCGGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC    9967389

```


Features in this part of subject sequence:
similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62
Identities = 33/39 (84%), Gaps = 0/39 (0%)
Strand=Plus/Minus

```

Query    1148      CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC    1186
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct    9967433    CGCCTCGGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC    9967395

```

>ref|NT_011387.8|Hs20_11544  Homo sapiens chromosome 20 genomic contig, reference assembly
Length=26259569

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY (sex determining region Y)-box 12

Score = 291 bits (322), Expect = 3e-75
Identities = 213/246 (86%), Gaps = 1/246 (0%)
Strand=Plus/Plus

```

Query    494      CCGGAGCTGGTGCAAGACCCCGAGTGGGCACATCAAGCGACCATGAACGCCITCATGGT    553
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct    246656    CCCG-GCTGGTGCAAGACCCCGAGCGGCCACATCAAGAGCCGATGAACGCATTTCATGGT    246714

Query    554      GTGGTCGCAGATCGAGCGGCGCAAGATCATGGAGCAGTCGCCCGACATGCACAACGCCGA    613
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct    246715    GTGGTCGCAGCAGCAACGGCGGAAGATCATGGACAGTGGCCCGACATGCACAACGCCGA    246774

Query    614      GATCTCCAAGCGGCTGGGCAACGCTGGAAGCTGCTCAAAGACAGCGACAAGATCCCTTT    673
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct    246775    GATCTCCAAGCGCTGGGCGCGCGCTGGCAGCTGCTGACGAGACTCGGAGAAGATCCCGTT    246834

Query    674      CATTTCGAGAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTA    733
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Sbjct    246835    CGTTCGGGAGGCGGAGCGGCTGCGGCTCAAGCACATGGCGGATTACCCGGACTACAAGTA    246894

Query    734      CCGGCC      739
          |||||
Sbjct    246895    CCGGCC      246900

```

Features in this part of subject sequence:

SRY (sex determining region Y)-box 12

Score = 131 bits (144), Expect = 5e-27
 Identities = 90/102 (88%), Gaps = 0/102 (0%)
 Strand=Plus/Plus

```
Query 1674 TCGCACTTCGAGTTCCTCCGGACTACTGCACGCCCCGAGGTGAGCGAGATGATCTCGGGAGAC 1733
          |||||||
Sbjct 247415 TCGCACTTCGAGTTCCTCCGGACTACTGCACCCCCGAGGTTACCGAGATGATCGCGGGGAC 247474

Query 1734 TGGCTCGAGTCCAGCATCTCCAACCTGGTTTTCACCTACTGA 1775
          |||||
Sbjct 247475 TGGCGCCCGTCTAGCATCGCAGACCTGGTTTTCACCTACTGA 247516
```

Features in this part of subject sequence:
 similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

```
Query 1148 CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
          |||||||
Sbjct 9955587 CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9955549
```

Features in this part of subject sequence:
 similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

```
Query 1148 CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
          |||||||
Sbjct 9955593 CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9955555
```

Features in this part of subject sequence:
 similar to hCG2045825


Score = 44.6 bits (48), Expect = 0.62
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

```
Query 1148 CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
          |||||||
Sbjct 9955599 CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9955561
```

Features in this part of subject sequence:
 similar to hCG2045825

Score = 44.6 bits (48), Expect = 0.62
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

```
Query 1148 CGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGC 1186
          |||||||
Sbjct 9955605 CGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGC 9955567
```

>ref|NW_001838084.2|Hs13_WGA793_36  Homo sapiens chromosome 13 genomic contig, alternate as
 (based on HuRef SCAF_1103279188152)
 Length=25468656

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features in this part of subject sequence:
 SRY-box 21

Score = 140 bits (154), Expect = 1e-29
 Identities = 164/219 (74%), Gaps = 2/219 (0%)

Features in this part of subject sequence:
SRY-box 15

Score = 129 bits (142), Expect = 2e-26
Identities = 158/213 (74%), Gaps = 2/213 (0%)
Strand=Plus/Minus

Query	528	AAGCGACCCATGAACGCCTTCATGGTGTGGT-CGCAGATCGAGCGGCGCAAGATCATGGA	586
Sbjct	7078179	AAGCGGCCGATGAACGCGTTTCATGGTGTGGAGCTCCGCTC-AGCGCCGCCAGATGGCGCA	7078121
Query	587	GCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAAACGCTGGAAGCT	646
Sbjct	7078120	GCAGAACCCCAAGATGCACAACATCCGAGATCTCCAAGCGGCTGGGCGCGCAGTGGGAAGCT	7078061
Query	647	GCTCAAAGACAGCGACAAGATCCCTTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCA	706
Sbjct	7078060	GCTGGACGAGGACGAGAAGCGGCCCTTCGTGGAGGAGGCCAAGCGGCTCCGCGCCCGACA	7078001
Query	707	CATGGCTGACTACCCCGACTACAAGTACCGGCC	739
Sbjct	7078000	CCTGCGCGACTACCCCGACTACAAGTACCGGCC	7077968

>ref|NT_010718.15|Hs17_10875 Homo sapiens chromosome 17 genomic contig, reference assembly
Length=21163833

Features in this part of subject sequence:
SRY-box 15

Score = 129 bits (142), Expect = 2e-26
Identities = 158/213 (74%), Gaps = 2/213 (0%)
Strand=Plus/Minus

Query	528	AAGCGACCCATGAACGCCTTCATGGTGTGGT-CGCAGATCGAGCGGCGCAAGATCATGGA	586
Sbjct	7090195	AAGCGGCCGATGAACGCGTTTCATGGTGTGGAGCTCCGCTC-AGCGCCGCCAGATGGCGCA	7090137
Query	587	GCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAAACGCTGGAAGCT	646
Sbjct	7090136	GCAGAACCCCAAGATGCACAACATCCGAGATCTCCAAGCGGCTGGGCGCGCAGTGGGAAGCT	7090077
Query	647	GCTCAAAGACAGCGACAAGATCCCTTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAGCA	706
Sbjct	7090076	GCTGGACGAGGACGAGAAGCGGCCCTTCGTGGAGGAGGCCAAGCGGCTCCGCGCCCGACA	7090017
Query	707	CATGGCTGACTACCCCGACTACAAGTACCGGCC	739
Sbjct	7090016	CCTGCGCGACTACCCCGACTACAAGTACCGGCC	7089984

>ref|NW_001838454.2|Hs17_WGAll163_36 Homo sapiens chromosome 17 genomic contig, alternate a
(based on HuRef SCAF_1103279188168)
Length=12595466

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
transcription factor SOX9

Score = 104 bits (114), Expect = 8e-19
Identities = 96/122 (78%), Gaps = 0/122 (0%)
Strand=Plus/Minus

Query	521	GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTTCGAGATCGAGCGGCGCAAGAT	580
Sbjct	5396434	GCACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGGCGCAGCGGCGCGCAGGAAGCT	5396375
Query	581	CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAAACGCTG	640
Sbjct	5396374	CGCGGACCAAGTACCGCACTTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAAGCTCTG	5396315
Query	641	GA	642
Sbjct	5396314	GA	5396313

Score = 59.0 bits (64), Expect = 3e-05
Identities = 70/95 (73%), Gaps = 0/95 (0%)
Strand=Plus/Minus

Features in this part of subject sequence:
 regulator of G-protein signaling 9 isoform 2
 regulator of G-protein signaling 9 isoform 1

```

Query    2050      CTGTGATTGTTGTTATTGATGTTGTTGTTGA      2080
          |||||
Sbjct    12330673  CTGTTGTTGTTGTTATTGCTGTTGTTGTTGA      12330703

```

Score = 41.0 bits (44), Expect = 7.5
Identities = 28/32 (87%), Gaps = 0/32 (0%)
Strand=Plus/Minus

```
Query    2051      TGTGATTGTTGTTATTGATGTTGTTGTTGATG      2082
          ||| ||||| ||||| ||| ||||| ||||| |||
Sbjct   10658531 TGTTATTGTTGTTGTTGCTGTTGTTGTTGTTG  10658500
```

```
>ref|NW_001838884.2|Hs3_WGA277_36 Homo sapiens chromosome 3 genomic contig, alternate asse  
(based on HuRef SCAF_1103279188385)  
Length=64955803
```

```
Sort alignments for this subject seq
E value   Score   Percent identity
Query start position   Subject star
```

Score = 104 bits (114), Expect = 8e-19
Identities = 161/224 (71%), Gaps = 12/224 (5%)
Strand=Plus/Minus

Query	522	CACATCAAGCGACCCATGAACGCCCTTCATGGTGTGGTCGAGATCGAGCGGGCGCAAGATC	581
Sbjct	56570764	CACATCAAGCGGGCCATGAACGCCCTTCATGGTATGGTCCCGGGCGCAGCGGGCGCAAGATG	56570705
Query	582	ATGGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG---CAAACGC	638
Sbjct	56570704	GCCCAGGAAAAACCCCAAGATGCACAACCTCGGAGATCAGCAACGCCTAGTGCCGAA---	56570648
Query	639	TGGAAGCTGC--TCAAAGACAGCGACAAGATCCCTTTCATTCTGA-GAGCGGAGCGGCTG	695
Sbjct	56570647	TGGAAGCTTCTGTCTCCGAGGCA--GAGAAGCGGCCATACA-TCGATGAAGCCCAAGCGGCTA	56570591
Query	696	CGCCTCAAGCACATGGCTGACTACCCCGCATCAAGTACCGCGG	739
Sbjct	56570590	CGCGCCACGACATGAAGGAGACCCCTGACTACAAGTACCGGACC	56570547

Features in this part of subject sequence:
sex-determining region Y-box 2

Score = 91.5 bits (100), Expect = 5e-15
 Identities = 153/219 (69%), Gaps = 2/219 (0%)
 Strand=Plus/Minus

```

Query    526      TCAAGCGACCCCATGAACGCCCTTCATGGTGTGGTTCGAGATCGAGCGGCGCAAGATCATGG 585
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    12593937  TCAAGCGGCCCATGAATGCCTTCATGGTGTGGTCCCGCGGCGAGCGGCGCAAGATGGCCC 12593878

Query    586      AGCAGTTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAACGCTGGAAGC 645
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    12593877  AGGAGAAACCCCAAGATGCACAACCTCGGAGATCAGCAAGCGCTGGGCGCCAGCTGGAAAC 12593818

Query    646      TGCTCAAGACAGCGACAAGATCCCTTTCATTCTGA-GAGGCGGAGCGGCTGCGCCTCAAG 704
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    12593817  TTTTGTCTGGAGACGGAGAACGCGCCGTTCA-TCGACGAGGCTAAGCGGCTGCGAGCGCTG 12593759

Query    705      CACATGGCTGACTACCCCGACTACAAGTACCGGCCCAAG 743
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    12593758  CACATGAAGGAGCACCCGGATTATAAATACCGGCCCGG 12593720
  
```

Features flanking this part of subject sequence:

368249 bp at 5' side: procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 isoform...
 1716439 bp at 3' side: hypothetical protein LOC205428

Score = 46.4 bits (50), Expect = 0.18
 Identities = 31/35 (88%), Gaps = 0/35 (0%)
 Strand=Plus/Plus

```

Query    2228      CATCACACCTTGGTTTTTGTATTTTGTCTTCTT 2262
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    48631837  CATCATCACTTTGGTTATGTTTATTTTGTCTTCTT 48631871
  
```

Features flanking this part of subject sequence:

555396 bp at 5' side: similar to peptidylprolyl isomerase A-like
 68809 bp at 3' side: butyrylcholinesterase precursor

Score = 42.8 bits (46), Expect = 2.2
 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Plus

```

Query    2055      ATTGTTGTTATTGATGTTGTTGTTGATG 2082
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    27830621  ATTGTTGTTGTTGTTGTTGTTGTTGATG 27830648
  
```

Features flanking this part of subject sequence:

8911 bp at 5' side: sterile alpha motif domain containing 7
 40774 bp at 3' side: leucine rich repeat containing 31

Score = 41.0 bits (44), Expect = 7.5
 Identities = 31/37 (83%), Gaps = 0/37 (0%)
 Strand=Plus/Plus

```

Query    2056      TTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAA 2092
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    24430482  TTGTTGTTATTGTTGTTGTTGTTGTTCTGCAAAAAATA 24430518
  
```


Features flanking this part of subject sequence:

360070 bp at 5' side: similar to hCG2021878
 1305561 bp at 3' side: hypothetical protein LOC131149

Score = 41.0 bits (44), Expect = 7.5
 Identities = 33/40 (82%), Gaps = 0/40 (0%)
 Strand=Plus/Minus

```

Query    180      TTCTCTCTTTACCCACCTCCGCCCTGCGAGGAGTTAGG 219
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    31502884  TTCTCTCTTTACCACTCAGCCGCTGCCAGGGGTTAGG 31502845
  
```

>ref|NT_010641.15|Hs17_10798  Homo sapiens chromosome 17 genomic contig, reference assembly
 Length=11472733

Sort alignments for this subject seq
 E value Score Percent identity

Query start position Subject star

Features in this part of subject sequence:
transcription factor SOX9

Score = 104 bits (114), Expect = 8e-19
Identities = 96/122 (78%), Gaps = 0/122 (0%)
Strand=Plus/Plus

```

Query 521      GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT 580
                |||
Sbjct 4044113  GCACGTCGAAGCGGCCCATGAACGCCTTCATGGTGTGGGCGCAGGCGGCGCAGGAAGCT 4044172

Query 581      CATGGAGCAGTCGCCCACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAAACGCTG 640
                |||
Sbjct 4044173  CGCGGACCACTACCCGACATTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAAGCTCTG 4044232

Query 641      GA 642
                ||
Sbjct 4044233  GA 4044234

```

Features in this part of subject sequence:
transcription factor SOX9


Score = 59.0 bits (64), Expect = 3e-05
Identities = 70/95 (73%), Gaps = 0/95 (0%)
Strand=Plus/Plus

```

Query 645      CTGCTCAAAGCAGCGACAAGATCCCTTTTCATTCGAGAGGCGGAGCGGCTGCGCCTCAAG 704
                |||
Sbjct 4045133  CTTCTGAACGAGAGCGAGAAGCGGCCCTTCGTGGAGGAGGCGGAGCGGCTGCGCGTGCAG 4045192

Query 705      CACATGGCTGACTACCCCGACTACAAGTACCGGCC 739
                |||
Sbjct 4045193  CACAAGAAGGACCCCGGATTACAAGTACCAGCC 4045227

```

>ref|NT_005612.15|Hs3_5769  Homo sapiens chromosome 3 genomic contig, reference assembly
Length=100530253

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY-box 14

Score = 104 bits (114), Expect = 8e-19
Identities = 161/224 (71%), Gaps = 12/224 (5%)
Strand=Plus/Plus

```

Query 522      CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATC 581
                |||
Sbjct 43978791  CACATCAAGCGGCCCATGAACGCCTTCATGGTATGGTCCCGGGGCGAGCGGCGCAAGATG 43978850

Query 582      ATGGAGCAGTCGCCCACATGCACAACGCCGAGATCTCCAAGCGGCTGGG---CAAACGC 638
                |||
Sbjct 43978851  GCCCAGGAAAACCCCAAGATGCACAACCTCGGAGATCAGCAACGCCTAGGTGCCGAA--- 43978907

Query 639      TGGAGCTGTC--TCAAAGACAGCGACAAGATCCCTTTTCATTCGA--GAGCGGAGCGGCTG 695
                |||
Sbjct 43978908  TGGAGCTTCTGTCCGAGGCA--GAGAAGCGGCCATACA--TCGATGAAGCCAAGCGGCTA 43978964

Query 696      CGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC 739
                |||
Sbjct 43978965  CGCGCCAGCACATGAAGGAGCACCTGACTACAAGTACCGACC 43979008

```

Features in this part of subject sequence:
sex-determining region Y-box 2

Score = 91.5 bits (100), Expect = 5e-15
Identities = 153/219 (69%), Gaps = 2/219 (0%)
Strand=Plus/Plus

```

Query 526      TCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG 585
                |||

```

```

Sbjct  87925420   TCAAGCGGCCCATGAATGCCCTTCATGGTGTGGTCCCGCGGGCAGCGGCCAAGATGGCCC 87925479
Query  586       AGCAGTCGCCCGACATGCACACGCCGAGATCTCCAAGCGGCTGGGCAACCGCTGGAAGC 645
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  87925480   AGGAGAAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGCGCCGAGTGGAAAC 87925539
Query  646       TGCICAAAGACAGCGACAAGATCCCTTTCATTCTGA-GAGGCGGAGCGGCTGCGCCTCAAG 704
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  87925540   TTTTGTCTGGAGACGGAGAAGCGGCCGCTTCA-TCGACGAGGCTAAGCGGCTGCGAGCGCTG 87925598
Query  705       CACATGGCTGACTACCCCGACTACAAGTACCGGCCAGG 743
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  87925599   CACATGAAGGAGCACCCGGATTATAAATACCGGCCCGG 87925637

```

Features flanking this part of subject sequence:

1479986 bp at 5' side: similar to PRO0419

371407 bp at 3' side: procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2 isoform...

Score = 46.4 bits (50), Expect = 0.18
 Identities = 31/35 (88%), Gaps = 0/35 (0%)
 Strand=Plus/Minus

```

Query  2228       CATCACCACCTTGGTTTGTGTTTATTTTGCTTCTT 2262
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  51912243   CATCATCACTTTGGTTATGTTTATTTTGTTTCTT 51912209

```

Features flanking this part of subject sequence:

680379 bp at 5' side: butyrylcholinesterase precursor

554392 bp at 3' side: hypothetical protein

Score = 42.8 bits (46), Expect = 2.2
 Identities = 26/28 (92%), Gaps = 0/28 (0%)
 Strand=Plus/Minus

```

Query  2055       ATTGTGTATTGATGTTGTTGTTGATG 2082
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  72724377   ATTGTGTGTTGTTGTTGTTGTTGATG 72724350

```

Features flanking this part of subject sequence:

51277 bp at 5' side: nuclear factor of kappa light polypeptide gene enhancer 1...

83898 bp at 3' side: hypothetical protein

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus

```

Query  2056       TTGTTGTTATTGATGTTGTTGTTGATG 2082
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  8124638   TTGTTGTTTGTGTTGTTGTTGTTGATG 8124664

```

Features in this part of subject sequence:
 hypothetical protein

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

```

Query  2056       TTGTTGTTATTGATGTTGTTGTTGATG 2082
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  20900949   TTGTTGTTATTGCTGTTGTTGTTGTTG 20900923

```

Features flanking this part of subject sequence:

1323998 bp at 5' side: hypothetical protein LOC131149

371774 bp at 3' side: similar to hCG2021878

Score = 41.0 bits (44), Expect = 7.5
 Identities = 33/40 (82%), Gaps = 0/40 (0%)
 Strand=Plus/Minus

```

Query  180       TTCTCTCTTTACCCACCTCCGCCCTGCGAGGAGTTGAGG 219
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct  69040917   TTCTCTCTTTACCCACTCAGCCGCTGCCAGGGGTTGAGG 69040878

```

Features flanking this part of subject sequence:

40760 bp at 5' side: leucine rich repeat containing 31
8896 bp at 3' side: sterile alpha motif domain containing 7

Score = 41.0 bits (44), Expect = 7.5
Identities = 31/37 (83%), Gaps = 0/37 (0%)
Strand=Plus/Minus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAAAA	2092
Sbjct	76123541	TTGTTGTTATTGTTGTTGTTGTTCTGAAAAATAA	76123505

>ref|NW_001842405.1|HsX_WGAL366.36 Homo sapiens chromosome X genomic contig, alternate ass
(based on HuRef SCAF_1103279188404)
Length=3857110

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY (sex determining region Y)-box 3

Score = 100 bits (110), Expect = 9e-18
Identities = 154/216 (71%), Gaps = 8/216 (3%)
Strand=Plus/Minus

Query	528	AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT---CATG	584
Sbjct	3649310	AAACGGCCCATGAACGCCTTCATGGTATGGTCCCGGGGCGAGCGGCGCAAAATGGCCCTG	3649251
Query	585	GAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAAACGCTGGAAG	644
Sbjct	3649250	GAGAAC---CCCAAGATGCACAATTCTGAGATCAGCAAGCGCTTGGGCGCCGACTGGAAA	3649194
Query	645	CTGCTCAAAGACAGCGACAAGATCCCTTTTCATTTCGA-GAGGCGGAGCGGCTGCGCCTCAA	703
Sbjct	3649193	CTGCTGACCGACGCCGAGACGACCATTCAT-CGACGAGGCGCAAGCGACTTCGCGCCGT	3649135
Query	704	GCACATGGCTGACTACCCCGACTACAAGTACCGGCC	739
Sbjct	3649134	GCACATGAAGGAGTATCCGGACTACAAGTACCGACC	3649099

Features flanking this part of subject sequence:
166860 bp at 5' side: zinc finger protein of the cerebellum 3
893562 bp at 3' side: fibroblast growth factor 13 isoform 1A

Score = 41.0 bits (44), Expect = 7.5
Identities = 28/32 (87%), Gaps = 0/32 (0%)
Strand=Plus/Plus

Query	2048	ACCTGTGATTGTTGTTATTGATGTTGTTGTTG	2079
Sbjct	882950	ACCTGTGATAGTTTTGTTGTTGTTGTTGTTG	882981

>ref|NT_011786.15|HsX_11943 Homo sapiens chromosome X genomic contig, reference assembly
Length=27718692

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY (sex determining region Y)-box 3

Score = 100 bits (110), Expect = 9e-18
Identities = 154/216 (71%), Gaps = 8/216 (3%)
Strand=Plus/Minus

Query	528	AAGCGACCCATGAACGCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGAT---CATG	584
Sbjct	23798156	AAACGGCCCATGAACGCCTTCATGGTATGGTCCCGGGGCGAGCGGCGCAAAATGGCCCTG	23798097
Query	585	GAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAAAACGCTGGAAG	644

```

Sbjct  23798096  GAGAAC---CCCAAGATGCACAATTCTGAGATCAGCAAGCGCTTGGGCGCCGACTGGAAA 23798040
Query   645      CTGCTCAAAGACAGCGACAAGATCCCTTTTCATTCTGA-GAGCGGAGCGGCTGCGCCTCAA 703
Sbjct  23798039  CTGCTGACCGACGCCGAGAGCGACCATTCAT-CGACGAGGCCAAGCGACTTCGCGCCGT 23797981
Query   704      GCACATGGCTGACTACCCCGACTACAAGTACCGGCC 739
Sbjct  23797980  GCACATGAAGGAGTATCCGACTACAAGTACCGACC 23797945

```

Features in this part of subject sequence:
dedicator of cytokinesis 11

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Minus

```

Query   1149      GCCITCGGCTCCGCTCCTTCGGCAGCC 1175
Sbjct  1898025  GCCITCGGCTCCGCTCCTTCGGCAGCC 1897999

```

Features flanking this part of subject sequence:
1062887 bp at 5' side: glutamate dehydrogenase 2
1072247 bp at 3' side: glutamate receptor 3 isoform flop precursor

Score = 41.0 bits (44), Expect = 7.5
Identities = 33/40 (82%), Gaps = 0/40 (0%)
Strand=Plus/Minus

```

Query   2056      TTGTGTATTGATGTGTGTGTGATGGCaaaaatssaaa 2095
Sbjct  5457504  TTGTGTGTGTGTGTGTGTGTGTGTGTTCAGAAAAACAAA 5457465

```

Features flanking this part of subject sequence:
168026 bp at 5' side: zinc finger protein of the cerebellum 3
894725 bp at 3' side: fibroblast growth factor 13 isoform 1B

Score = 41.0 bits (44), Expect = 7.5
Identities = 28/32 (87%), Gaps = 0/32 (0%)
Strand=Plus/Plus

```

Query   2048      ACCTGTGATTGTTGTTATTGATGTTGTGTTG 2079
Sbjct  21031603  ACCGTGTGATGTTTGTGTGTGTGTGTGTTG 21031634

```

>ref|NT_027140.6|Hs13_27300 Homo sapiens chromosome 13 genomic contig, reference assembly
Length=1821999

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY (sex determining region Y)-box 1

Score = 96.9 bits (106), Expect = 1e-16
Identities = 152/215 (70%), Gaps = 2/215 (0%)
Strand=Plus/Plus

```

Query   526      TCAAGCGACCCATGAACGCCITTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGG 585
Sbjct  218130  TCAAACGCGCCATGAACGCCITTCATGGTGTGGTCCCGCGGGCAGCGGCGCAAGATGCCCC 218189
Query   586      AGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAACGCTGGAAGC 645
Sbjct  218190  AGGAGAACCCCAAGATGCACAACTCGGAGATCAGCAAGCGCCTGGGGGCCGAGTGGGAAGG 218249
Query   646      TGCTCAAAGACAGCGACAAGATCCCTTTTCATTCTGA-GAGCGGAGCGGCTGCGCCTCAAG 704
Sbjct  218250  TCATGTCCGAGGCCGAGAGCGGCCGTTCA-TCGACGAGGCCAAGCGGCTGCGCGCGCTG 218308
Query   705      CACATGGCTGACTACCCGACTACAAGTACCGGCC 739
Sbjct  218250  CACATGGCTGACTACCCGACTACAAGTACCGGCC 739

```

Sbjct 218309 CACATGAAGGAGCACCCGATTACAAGTACCGGCC 218343

Features flanking this part of subject sequence:

269051 bp at 5' side: SRY (sex determining region Y)-box 1
38475 bp at 3' side: hypothetical protein LOC122258

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

Query 2056 TTGTTGTTATTGATGTTGTTGTTGAT 2082
||||||| ||||||||| ||
Sbjct 488205 TTGTTGTTGTTGATGTTGTTGTTG 488231

>ref|NW_001838745.1|Hs22_WGA1304_36 Homo sapiens chromosome 22 genomic contig, alternate a
(based on HuRef SCAF_1103279188372)
Length=21026802

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY (sex determining region Y)-box 10

Score = 95.1 bits (104), Expect = 4e-16
Identities = 94/122 (77%), Gaps = 0/122 (0%)
Strand=Plus/Minus

Query 521 GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGCTCGAGATCGAGCGGCGCAAGAT 580
||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||
Sbjct 16472614 GCACGTCAAGCGGCCCATGAACGCCTTCATGGTGTGGGCTCAGGCAGCGCAGGAAGCT 16472555
Query 581 CATGGAGCAGTCGCGCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAACGCTG 640
||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||
Sbjct 16472554 CGCGGACCAAGTACCCGCACCTGCACAACGCTGAGCTCAGCAAGACGCTGGGCAAGCTCTG 16472495
Query 641 GA 642
||
Sbjct 16472494 GA 16472493

Features in this part of subject sequence:
SRY (sex determining region Y)-box 10

Score = 77.0 bits (84), Expect = 1e-10
Identities = 79/101 (78%), Gaps = 2/101 (1%)
Strand=Plus/Minus

Query 644 GCTGCTCAAAGACAGCGACAAGATCCCTTTTCATTTCGAG-AGGCGGAGCGGCTGCGCTCA 702
||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||
Sbjct 16467270 GCTGCTGAACGAAAGTGACAAGCGCCCTTCAT-CGAGGAGGCTGAGCGGCTCCGTATGC 16467212
Query 703 AGCACATGGCTGACTACCCCGACTACAAGTACCGGCCAGG 743
||||||| ||||||||| ||||||||| ||||||||| ||||||||| ||
Sbjct 16467211 AGCACAAGAAAGACACCCGGACTACAAGTACCAGGCCAGG 16467171

Features flanking this part of subject sequence:
22174 bp at 5' side: like-glycosyltransferase
1289151 bp at 3' side: intestine-specific homeobox

Score = 42.8 bits (46), Expect = 2.2
Identities = 25/26 (96%), Gaps = 0/26 (0%)
Strand=Plus/Plus

Query 2056 TTGTTGTTATTGATGTTGTTGTTGAT 2081
||||||| ||||||||| ||||||||| ||
Sbjct 12263566 TTGTTGTTATTGTTGTTGTTGTTGAT 12263591

Features in this part of subject sequence:
calcineurin binding protein 1

Score = 41.0 bits (44), Expect = 7.5

7/16/08

```
Sort alignments for this subject seq
E value   Score   Percent identity
Query start position   Subject star
```

```
Sort alignments for this subject seq
E value   Score  Percent identity
Query start position  Subject star
```

(based on HuRef SCAF_1103279188181)
Length=2624016

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:

SRY (sex determining region Y)-box 8

Score = 86.0 bits (94), Expect = 2e-13
Identities = 83/107 (77%), Gaps = 0/107 (0%)
Strand=Plus/Minus

```
Query 528      AAGCGACCCATGAACGCCCTTCATGGTGTGGTCGCAGATCGAGCGGCGCAAGATCATGGAG 587
                |||||
Sbjct 1665887  AAGCGGCCCATGAACGCATTTCATGGTGTGGGCGCAGGCGCGCGCCGAAGCTGGCCGAC 1665828
                |||||
Query 588      CAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAA 634
                |||||
Sbjct 1665827  CAGTACCCGACCTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAA 1665781
                |||||
```

Features in this part of subject sequence:

SRY (sex determining region Y)-box 8

Score = 53.6 bits (58), Expect = 0.001
Identities = 71/99 (71%), Gaps = 6/99 (6%)
Strand=Plus/Minus

```
Query 681      GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTAC----- 734
                |||||
Sbjct 1664351  GAGGCAGAGCGCCTTCGCGTGCAGCACAGAAGGACCACCCCGACTACAAGTACCAGCCA 1664292
                |||||
Query 735      CGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCC 773
                |||||
Sbjct 1664291  CGGCGCAGGAAGAGCGCCAAAGCCGGCCACAGCGACTCC 1664253
                |||||
```

>ref|NT_037887.4|Hs16_37891 Homo sapiens chromosome 16 genomic contig, reference assembly
Length=8576922

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:

SRY (sex determining region Y)-box 8

Score = 86.0 bits (94), Expect = 2e-13
Identities = 83/107 (77%), Gaps = 0/107 (0%)
Strand=Plus/Plus

```
Query 528      AAGCGACCCATGAACGCCCTTCATGGTGTGGTGCAGATCGAGCGGCGCAAGATCATGGAG 587
                |||||
Sbjct 972230  AAGCGGCCCATGAACGCATTTCATGGTGTGGGCGCAGGCGGCGCGCCGAAGCTGGCCGAC 972289
                |||||
Query 588      CAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAA 634
                |||||
Sbjct 972290  CAGTACCCGACCTGCACAACGCCGAGCTCAGCAAGACGCTGGGCAA 972336
                |||||
```

Features in this part of subject sequence:

SRY (sex determining region Y)-box 8

Score = 53.6 bits (58), Expect = 0.001
Identities = 71/99 (71%), Gaps = 6/99 (6%)
Strand=Plus/Plus

```
Query 681      GAGGCGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTAC----- 734
                |||||
Sbjct 973766  GAGGCAGAGCGCCTTCGGGTGCAGCACAGAAGGACCACCCCGACTACAAGTACCAGCCA 973825
                |||||
Query 735      CGGCCAGGAAGAAGGTGAAGTCCGGCAACGCCAACTCC 773
                |||||
Sbjct 973826  CGGCGCAGGAAGAGCGCCAAAGCCGGCCACAGCGACTCC 973864
                |||||
```

```
Sort alignments for this subject seq
E value   Score   Percent identity
Query start position   Subject star
```

Features in this part of subject sequence:

hypothetical protein


Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus

```
Query   2423      CCTtttttCCTCCTCTTTTCCCTT   2449
                || ||||| ||||| ||||| |||||
Sbjct   28353580  CCATTTTTTCCTGCCTCTTTCCCTT   28353606
```

Features in this part of subject sequence:
 astroactin isoform 1

Score = 41.0 bits (44), Expect = 7.5
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Plus

```
Query   2290      GCACCCCTaccacccctttttt   2311
                ||||| ||||| ||||| |||||
Sbjct   28766569  GCACCCCTCCCCCCTTTTTT    28766590
```

>ref|NW_001838085.1|Hs13_WGA794_36  Homo sapiens chromosome 13 genomic contig, alternate as
 (based on HuRef SCAF_1103279188104)
 Length=1807819

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features flanking this part of subject sequence:
 287495 bp at 3' side: hypothetical protein LOC122258

Score = 77.0 bits (84), Expect = 1e-10
 Identities = 80/105 (76%), Gaps = 0/105 (0%)
 Strand=Plus/Plus


```
Query   526      TCAAGCGACCCATGAACGCCCTTCATGGTGTGGTCGCAGATCAGCGGCGCAAGATCATGG   585
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   226768    TCAAACGGCCCATGAACGCCCTTCATGGTGTGGTCCCGCGGCGCAGCGGCGCAAGATGCCCC   226827

Query   586      AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGG   630
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   226828    AGGAGAACCCCAAGATGCACAACCTCGGAGATCAGCAAGCGCCTGG   226872
```

Features flanking this part of subject sequence:
 39257 bp at 3' side: hypothetical protein LOC122258

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus

```
Query   2056      TTGTGTGTTATGATGTTGTTGTTGATG   2082
                ||||| ||||| ||||| ||||| |||||
Sbjct   475084    TTGTGTGTTGTTGATGTTGTTGTTGTTG   475110
```

>ref|NT_004487.18|Hs1_4644  Homo sapiens chromosome 1 genomic contig, reference assembly
 Length=56413061

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features in this part of subject sequence:
 SRY-box 13

Score = 77.0 bits (84), Expect = 1e-10
 Identities = 73/91 (80%), Gaps = 2/91 (2%)
 Strand=Plus/Plus

```
Query   522      CACATCAAGCGACCCATGAACGCCCTTCATGGTGTGGTCGCAGATCAGCGGCGCAAGATC   581
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct   54583178  CACATCAAGAGGCCCATGAACGCCCTTCATGGTGTGGGCGAAGGATGAGCGGAGGAAGATC   54583237
```

```

Query    582          ATG-GAGCAGTCGCCCGACATGCACAACGCC    611
          ||  |||  ||  ||  |||||  |||||  |||
Sbjct    54583238      CTGCAAGCCTTC--CCAGACATGCACAACCTCC    54583267

```

Features in this part of subject sequence:

protein phosphatase 1, regulatory (inhibitor) subunit 12B...
protein phosphatase 1, regulatory (inhibitor) subunit 12B...

Score = 46.4 bits (50), Expect = 0.18
Identities = 34/40 (85%), Gaps = 0/40 (0%)
Strand=Plus/Plus

```

Query    2056          TTGTTGTTATTGAIGTTGTTGTTGATGGC 2095
          |||||  |||  |||  |||||  |||  |||||  |||
Sbjct    52810695      TTGTTGTTGTTGTTGTTGTTGTTGTTGTTTAAAAA 52810734

```

Features in this part of subject sequence:

protein phosphatase 1, regulatory (inhibitor) subunit 12B...
protein phosphatase 1, regulatory (inhibitor) subunit 12B...

Score = 46.4 bits (50), Expect = 0.18
Identities = 34/40 (85%), Gaps = 0/40 (0%)
Strand=Plus/Plus

```

Query    2056          TTGTTGTTATTGAIGTTGTTGTTGATGGC 2095
          |||||  |||  |||  |||||  |||  |||||  |||
Sbjct    52810698      TTGTTGTTGTTGTTGTTGTTGTTGTTTAAAAA 52810737

```

Features flanking this part of subject sequence:

327837 bp at 5' side: hypothetical protein LOC116461
76799 bp at 3' side: chromosome 1 open reading frame 21

Score = 42.8 bits (46), Expect = 2.2
Identities = 26/28 (92%), Gaps = 0/28 (0%)
Strand=Plus/Plus

```

Query    2056          TTGTTGTTATTGAIGTTGTTGTTGATGG 2083
          |||||  |||  |||  |||||  |||  |||||  |||
Sbjct    34860172      TTGTTGTTGTTGTTGTTGTTGTTGTTGATGG 34860199

```

Features in this part of subject sequence:

astrotactin isoform 1
astrotactin isoform 2

Score = 41.0 bits (44), Expect = 7.5
Identities = 22/22 (100%), Gaps = 0/22 (0%)
Strand=Plus/Minus

```

Query    2290          GCACCCCTccccccctttttt 2311
          |||||  |||||  |||||  |||||  |||||
Sbjct    27602408      GCACCCCTCCCCCCTTTTTT 27602387

```

Features in this part of subject sequence:

hypothetical protein

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Minus

```

Query    2423          CCTtttttCCTCCTCTTTTCCCTT 2449
          ||  |||||  |||  |||||  |||||  |||||
Sbjct    28014783      CCATTTTTTCTGCTCTTTTCCCTT 28014757

```

Features flanking this part of subject sequence:

409150 bp at 5' side: family with sequence similarity 5, member C
1294572 bp at 3' side: regulator of G-protein signalling 18

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```

Query    2056      TTGTTGTTATTGATGTTGTTGTTGATG    2082
          |||
Sbjct    41323524  TTGTTGTTATTGTTGTTGTTGTTGTTG    41323550

```

Features flanking this part of subject sequence:

409171 bp at 5' side: family with sequence similarity 5, member C
1294551 bp at 3' side: regulator of G-protein signalling 18

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```

Query    2056      TTGTTGTTATTGATGTTGTTGTTGATG    2082
          |||
Sbjct    41323545  TTGTTGTTATTGTTGTTGTTGTTGTTG    41323571

```

>ref|NW_001839132.1|Hs8_WGA525_36 Homo sapiens chromosome 8 genomic contig, alternate asse
(based on HuRef SCAF_1103279188282)
Length=30141836

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY-box 17

Score = 66.2 bits (72), Expect = 2e-07
Identities = 50/59 (84%), Gaps = 0/59 (0%)
Strand=Plus/Plus

```

Query    681      GAGGCGGAGCGGCTGCGCCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC    739
          |||
Sbjct    7238558  GAGGCGAGCGGCTGCGCGTGCAGCACATGCAGGACCACCCCACTACAAGTACCGGCC    7238616

```

Features in this part of subject sequence:
SRY-box 17

Score = 55.4 bits (60), Expect = 3e-04
Identities = 76/105 (72%), Gaps = 6/105 (5%)
Strand=Plus/Plus

```

Query    530      GCGACCCATGAACGCCCTTCATGGTGTGGTCGAGATCGAGCGGCGCAAGATCATGG---A    586
          |||
Sbjct    7237795  GCGGCCGATGAACGCCTTCATGGTGTGGGCTAAGGACGA---GCGCAAGCGGTGGCGCA    7237851
Query    587      GCAGTCGCCCCACATGCACAAACGCCGAGATCTCCAAGCGGCTGGG    631
          |||
Sbjct    7237852  GCAGAATCCAGACCTGCACAAACGCCGAGTTGAGCAAGATGCTGGG    7237896

```

Features in this part of subject sequence:
hypothetical protein LOC23514

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```

Query    2056      TTGTTGTTATTGATGTTGTTGTTGATG    2082
          |||
Sbjct    497262  TTGTTGTTATTGTTGTTGTTGTTGTTG    497288

```

Features in this part of subject sequence:
hypothetical protein LOC23514

Score = 41.0 bits (44), Expect = 7.5
Identities = 30/35 (85%), Gaps = 0/35 (0%)
Strand=Plus/Plus

```

Query    2051      TGTGATTGTTGTTATTGATGTTGTTGTTGATGGCA    2085
          |||
Sbjct    497266  TGTTATTGTTGTTGTTGTTGTTGTTGTTGTTGACA    497300

```

63747 bp at 5' side: ganglioside-induced differentiation-associated protein 1 ...
181279 bp at 3' side: similar to hCGI799828

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATG	2082
Sbjct	27230124	TTGTTGTTATTGTTGTTGTTGTTGTTG	27230098

473228 bp at 5' side: cysteine-rich secretory protein LCCL domain containing 1
33133 bp at 3' side: hepatocyte nuclear factor 4, gamma

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATG	2082
Subject	28305493	TTGTTGTTGTTGTTGTTGTTGTTGATG	28305467

```
Sort alignments for this subject seq
E value   Score   Percent identity
Query start position   Subject star
```

Score = 66.2 bits (72), Expect = 2e-07
Identities = 50/59 (84%), Gaps = 0/59 (0%)
Strand=Plus/Plus

Query	681	GAGGCGGAGCGGCTGCGCCTCAAGCACATGGTGACTACCCCGACTACAAGTACCGGCC	739
Spjct	7225020	GAGGCAGAGCGGCTGCGCGTGCAGCACATGCAGGACCACCCCAACTACAAGTACCGGCC	7225078

Features in this part of subject sequence:
SRY-box 17

Score = 55.4 bits (60), Expect = 3e-04
Identities = 76/105 (72%), Gaps = 6/105 (5%)
Strand=Plus/Plus

```

Query    530      GCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGGCGCAAGATCATGG---A   586
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct    7224257   GCGGGCGATGAACGCTTTCATGGTGTGGGCTAAGACGGA---GCGCAAAGCGGCTGGCGCA 7224313

Query    587      GCAGTCGCCCGACATGCAACAACGCCGAGATCTCCAAGCGGCTGGG   631
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct    7224314   GCAGAATCCAGACCTGCACAACGCCGAGTTGAGCAAGATGCTGGG   7224358

```

63856 bp at 5' side: ganglioside-induced differentiation-associated protein 1 ...
184610 bp at 3' side: similar to hCGI799828 isoform 1

```

Query    2051      TGTGATTGTTGTTATTGATGTTGTTGTTGATGGCAA      2086
          ||| ||||| ||| ||| ||||| ||| |||
Sbjct    27193847 TGTTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTAGCAA      27193812

```

Features in this part of subject sequence:
hypothetical protein LOC23514

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATG	2082
Subject	488931	TTGTTGTTATTGTTGTTGTTGTTGTTG	488957

Score = 41.0 bits (44), Expect = 7.5
Identities = 30/35 (85%), Gaps = 0/35 (0%)
Strand=Plus/Plus

```

Query    2051      TGTGATTGTTGTTATTGATGTTGTTGTTGATGGCA      2085
          |||      |||      |||      |||      |||      |||      |||
Sbjct    488935    TGTTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGACA    488969

```

Features flanking this part of subject sequence:
63869 bp at 5' side: ganglioside-induced differentiation-associated protein 1 ...
184606 bp at 3' side: similar to hCG1799828 isoform 1

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Minus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATG	2082
Sbjct	27193851	TTGTTGTTATTGTTGTTGTTGTTGTTG	27193825

Features flanking this part of subject sequence:
474603 bp at 5' side: cysteine-rich secretory protein LCCL domain containing 1
33122 bp at 3' side: hepatocyte nuclear factor 4, gamma

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Minus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
            |||||
Sbjct 28272460 TTGTTGTTGTTGTTGTTGTTGTTGATG 28272434
```

```
>ref|NW_001842422.1|HsY_WGAL383_36 Homo sapiens chromosome Y genomic contig, alternate ass
(based on HuRef SCAF_1103279188414)
Length=3942718
```

```
Sort alignments for this subject seq
E value   Score   Percent identity
Query start position   Subject star
```

Features in this part of subject sequence:
sex determining region Y

Score = 64.4 bits (70), Expect = 7e-07
Identities = 94/126 (74%), Gaps = 8/126 (6%)
Strand=Plus/Minus

Query	528	AAGCGACCCATGAACGCCTTCATGGTGTGGTCGC-AGATCAGAGCGGCGCAAGAT---CAT	583
Sbjct	8468	AAGCGACCCATGAACGCATTCATCGTGTGGTCTCGCGATC-AGAGCGCAAGATGGCTCT	8410
Query	584	GGAGCAGTCGCCCGACATGCACAACGCCAGATCTCCAAGCGGCTGGGCAAAACGCTGGAA	643
Sbjct	8409	AGAG-AATC-CCAGA-ATGCGAAATCAGAGATCAGCAAGCAGCTGGGATACCAGTGGAA	8353
Query	644	GCTGCT	649
Sbjct	8352	AATGCT	8347

Features flanking this part of subject sequence:

770513 bp at 5' side: TGF β -induced factor homeobox 2-like, Y-linked
 776921 bp at 3' side: hypothetical protein

Score = 44.6 bits (48), Expect = 0.62
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

Query 1149 GCCTCGGCCTCCGCTCCTCGGCAGCCTCGGCCTCCGCA 1187
 |||||
 Sbjct 1579134 GCCTCGGCCTCTGCCTCCACCTCAGCCTCTGCCTCCACA 1579096

>ref|NT_011896.9|HsY_12053 Homo sapiens chromosome Y genomic contig, reference assembly
 Length=6265435

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features in this part of subject sequence:
 sex determining region Y

Score = 64.4 bits (70), Expect = 7e-07
 Identities = 94/126 (74%), Gaps = 8/126 (6%)
 Strand=Plus/Minus

Query 528 AAGCGACCCATGAACGCTTCATGGTGTGGTCGC-AGATCGAGCGCGCAAGAT---CAT 583
 |||||
 Sbjct 5944 AAGCGACCCATGAACGCAATTCATCGTGTGGTCTCGCGATC-AGAGCGCAAGATGGCTCT 5886
 Query 584 GGAGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGGCAACGCTGGAA 643
 |||||
 Sbjct 5885 AGAG-AATC-CCAGA-ATGCGAACTCAGAGATCAGCAAGCAGCTGGGATACCACTGGAA 5829
 Query 644 GCTGCT 649
 |||||
 Sbjct 5828 AATGCT 5823

Features flanking this part of subject sequence:
 675817 bp at 5' side: TGF β -induced factor homeobox 2-like, Y-linked
 777040 bp at 3' side: protocadherin 11 Y-linked isoform a

Score = 44.6 bits (48), Expect = 0.62
 Identities = 33/39 (84%), Gaps = 0/39 (0%)
 Strand=Plus/Minus

Query 1149 GCCTCGGCCTCCGCTCCTCGGCAGCCTCGGCCTCCGCA 1187
 |||||
 Sbjct 1474178 GCCTCGGCCTCTGCCTCCACCTCAGCCTCTGCCTCCACA 1474140

Features in this part of subject sequence:
 transducin beta-like 1Y
 transducin beta-like 1Y


Score = 42.8 bits (46), Expect = 2.2
 Identities = 31/36 (86%), Gaps = 0/36 (0%)
 Strand=Plus/Plus

Query 2047 GACCTGIGATTGTTGTTATTGATGTTGTTGTTGATG 2082
 || ||||
 Sbjct 4284860 GAACCTGTTTTGTTGTTATTGTTGTTGTTGTTGTTG 4284895

Features in this part of subject sequence:
 transducin beta-like 1Y
 transducin beta-like 1Y

Score = 41.0 bits (44), Expect = 7.5
 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query 2051 TGTGATGTTGTTATTGATGTTGTTGTTGATG 2082
 ||| |||||
 Sbjct 4284873 TGTATTGTTGTTGTTGTTGTTGTTGTTGTTG 4284904

>ref|NT_011333.5|Hs20_11490  Homo sapiens chromosome 20 genomic contig, reference assembly
Length=1702150

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
hypothetical protein
SRY-box 18

Score = 62.6 bits (68), Expect = 2e-06
Identities = 83/114 (72%), Gaps = 6/114 (5%)
Strand=Plus/Minus


```
Query 521      GCACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGGCGCAAGAT 580
              || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1417251  GCGCATCCGGCGGCCCATGAACGCCTTCATGGTGTGGGCAAGGACGA---GCGCAAGCG 1417195

Query 581      CATGG---AGCAGTCGCCCGACATGCACAACGCCGAGATCTCCAAGCGGCTGGG 631
              ||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1417194  GCTGGCTCAGCAGAACCCGGACCTGCACAACGCGGTGCTCAGCAAGATGCTGGG 1417141
```

Features in this part of subject sequence:
hypothetical protein
SRY-box 18

Score = 53.6 bits (58), Expect = 0.001
Identities = 47/59 (79%), Gaps = 0/59 (0%)
Strand=Plus/Minus

```
Query 681      GAGCGGGAGCGGCTGCGCCTCAAGCACATGGCTGACTACCCCGACTACAAGTACCGGCC 739
              || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 1416895  GAAGCCGAACGGCTGCGCGTGCAGCACTTGCGCGACCAACCCCAACTACAAGTACCGGCC 1416837
```

>ref|NW_001838052.1|Hs12_WGA761_36  Homo sapiens chromosome 12 genomic contig, alternate as
(based On HuRef SCAF_1103279188408)
Length=21675488

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY (sex determining region Y)-box 5 isoform c
SRY (sex determining region Y)-box 5 isoform b

Score = 57.2 bits (62), Expect = 1e-04
Identities = 76/103 (73%), Gaps = 2/103 (1%)
Strand=Plus/Minus

```
Query 522      CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTC-GCAGATCGAGCGGCGCAAGAT 580
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 14103106  CACATAAAGCGTCCAATGAATGCCCTTCATGGTGTGGGCTAAAGAT-GAACGAGAAAGAT 14103048

Query 581      CATGGAGCAGTCGCCCCGACATGCACAACGCCGAGATCTCCAAG 623
              || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 14103047  CCTTCAAGCCTTTCTTGACATGCACAACCTCCAACATCAGCAAG 14103005
```

Features flanking this part of subject sequence:
15642 bp at 5' side: hypothetical protein LOC440087
585 bp at 3' side: hypothetical protein LOC144608

Score = 42.8 bits (46), Expect = 2.2
Identities = 29/33 (87%), Gaps = 0/33 (0%)
Strand=Plus/Minus

```
Query 2050      CTGIGATTGTTGTTATTGATGTGTGTTGTTGATG 2082
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 5384229  CTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTG 5384197
```

Features flanking this part of subject sequence:
70138 bp at 5' side: plectstrin homology domain containing, family A member 5

Features flanking this part of subject sequence:

1925 bp at 5' side: TRM1 tRNA methyltransferase 1
16847 bp at 3' side: transcriptional repressor NAC1

Score = 51.8 bits (56), Expect = 0.004
Identities = 34/38 (89%), Gaps = 0/38 (0%)
Strand=Plus/Minus


```
Query 1149      GCCTCGGCCTCCGCCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                |||||
Sbjct 4491977   GCCTCGGCCTCCGCCCTCCGCCCTCCGCCCTCCGC 4491940
```

Features in this part of subject sequence:

calcium channel, alpha 1A subunit isoform 2
calcium channel, alpha 1A subunit isoform 1

Score = 41.0 bits (44), Expect = 7.5
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Minus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGA 2080
                |||||
Sbjct 4698340   TTGTTGTTGTTGATGTTGTTGTTGA 4698316
```

>ref|NT_023133.12|Hs5_23289  Homo sapiens chromosome 5 genomic contig, reference assembly
Length=25714846

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features flanking this part of subject sequence:

3698 bp at 5' side: NK2 transcription factor related, locus 5
79019 bp at 3' side: stanniocalcin 2 precursor

Score = 51.8 bits (56), Expect = 0.004
Identities = 42/50 (84%), Gaps = 2/50 (4%)
Strand=Plus/Plus

```
Query 1137      CGGACTCCCAGCGCCTCCGCCCTCCTCGGCAGCCTCGGCCTCCGC 1186
                |||||
Sbjct 17475370   CGGACTCCCAGC--CTCGGCCTCCGCCCTCCGCCCTCCGCCCTCCGC 17475417
```

Features in this part of subject sequence:
slit homolog 3

Score = 44.6 bits (48), Expect = 0.62
Identities = 32/36 (88%), Gaps = 1/36 (2%)
Strand=Plus/Minus

```
Query 2423      CCTtttttCCTCCCTCTTTTCC-CCTGCCCCCTC 2457
                |||||
Sbjct 13112345   CCTTTTTTCTCCCTCTTATCCTCCCTCCGCCCTC 13112310
```

Features flanking this part of subject sequence:

60329 bp at 5' side: HMP19 protein
556789 bp at 3' side: msh homeobox 2

Score = 42.8 bits (46), Expect = 2.2
Identities = 32/38 (84%), Gaps = 0/38 (0%)
Strand=Plus/Plus

```
Query 1999      CTCTGCCAGCCGGAGGGACGCGGAGGAGGAAGAGGGT 2036
                |||||
Sbjct 18404423   CTCTGCACAGCCGGACAGGTGAGGAGGAGGAAGAGGGT 18404460
```

Features in this part of subject sequence:

SRX (sex determining region Y)-box 30 isoform a
SRX (sex determining region Y)-box 30 isoform b

(based on HuRef SCAF_1103279188395)
Length=20933881

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features flanking this part of subject sequence:
699382 bp at 5' side: myocyte enhancer factor 2C
378040 bp at 3' side: hypothetical protein

Score = 50.0 bits (54), Expect = 0.014
Identities = 35/40 (87%), Gaps = 0/40 (0%)
Strand=Plus/Minus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATGGC	2095
Sbjct	18105201	TTGTTGTTGTTGTTGTTGTTGATAGAAACAAAAA	18105162

Features flanking this part of subject sequence:
1347233 bp at 5' side: EGF-like repeats and discoidin I-like domains-containing ...
881684 bp at 3' side: cytochrome c oxidase subunit VIIc precursor

Score = 44.6 bits (48), Expect = 0.62
Identities = 33/39 (84%), Gaps = 0/39 (0%)
Strand=Plus/Plus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATGGCAAAAAA	2094
Sbjct	14316178	TTGTTGTTATTGTTGTTCTATTATGTTAAAAA	14316216

>ref|NW_001838865.2|Hs2_WGA258_36 Homo sapiens chromosome 2 genomic contig, alternate asse
(based on HuRef SCAF_1103279188138)
Length=7557636

Features flanking this part of subject sequence:
283252 bp at 5' side: hypothetical protein LOC79843
116307 bp at 3' side: plasminogen activator inhibitor type 1, member 2

Score = 50.0 bits (54), Expect = 0.014
Identities = 35/40 (87%), Gaps = 0/40 (0%)
Strand=Plus/Plus

Query	2047	GACCTGIGATTGTTGTTATTGATGTTGTTGATGGCAA	2086
Sbjct	1525080	GACCTGGGATTTTGTGTTGTTGTTGTTGTTGTTGCAA	1525119

>ref|NT_006576.15|Hs5_6733 Homo sapiens chromosome 5 genomic contig, reference assembly
Length=46378398

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features flanking this part of subject sequence:
1500958 bp at 5' side: hypothetical protein
319712 bp at 3' side: cadherin 18, type 2 preproprotein

Score = 50.0 bits (54), Expect = 0.014
Identities = 27/27 (100%), Gaps = 0/27 (0%)
Strand=Plus/Minus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATG	2082
Sbjct	19126380	TTGTTGTTATTGATGTTGTTGTTGATG	19126354

Features flanking this part of subject sequence:
2372 bp at 5' side: hypothetical protein
695213 bp at 3' side: hypothetical protein

Score = 41.0 bits (44), Expect = 7.5
Identities = 28/32 (87%), Gaps = 0/32 (0%)
Strand=Plus/Minus

```

Query    2628      GGGGAGCTGGCGGCGCGGCTGCTGGGCCTCC 2659
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    1877085  GGGGAGCGGGCGCGCGCGGCTGCGCGACTCC 1877054

```

Features in this part of subject sequence:
KPL2 protein isoform 1

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```

Query    2052      GTGATTGTTGTTATTGATGTTGTTGTT 2078
          ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    35740888  GTGGTTGTTGTTATTGTTGTTGTTGTT 35740914

```

>ref|NT_009237.17|Hs11_9394 Homo sapiens chromosome 11 genomic contig, reference assembly
Length=49571094

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
SRY (sex determining region Y)-box 6 isoform 2
SRY (sex determining region Y)-box 6 isoform 1

Score = 50.0 bits (54), Expect = 0.014
Identities = 65/90 (72%), Gaps = 0/90 (0%)
Strand=Plus/Minus

```

Query    522      CACATCAAGCGACCCATGAACGCCTTCATGGTGTGGTCGAGATCGAGCGGCGCAAGATC 581
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    14797892  CACATTAAGCGACCAATGAATGCATTGTTGTTGGGCAAGGATGAGAGGAGAAAAATC 14797833

Query    582      ATGAGGACAGTCGCCCCGACATGCACAACGCC 611
          ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    14797832  CTTAGGCCCTTCCCGGACATGCATAATCC 14797803

```

Features flanking this part of subject sequence:
193583 bp at 5' side: leucine zipper protein 2
1060010 bp at 3' side: transmembrane protein 16C

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```

Query    2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    24081028  TTGTTGTTGTTGTTGTTGTTGTTGATG 24081054

```

Features flanking this part of subject sequence:
13517 bp at 5' side: cryptochrome 2 (photolyase-like)
33 bp at 3' side: mitogen-activated protein kinase 8 interacting protein 1

Score = 41.0 bits (44), Expect = 7.5
Identities = 35/42 (83%), Gaps = 1/42 (2%)
Strand=Plus/Plus

```

Query    1155      GCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGCGCTCGCG 1196
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct    44694540  GCCTCCGCCTCCTTCGCGAGCGCCGCTCCTCCGCGC-CGCG 44694580

```

>ref|NT_007819.16|Hs7_7976 Homo sapiens chromosome 7 genomic contig, reference assembly
Length=47690382

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features flanking this part of subject sequence:
627203 bp at 5' side: Sp8 transcription factor isoform 2
15247 bp at 3' side: Sp4 transcription factor

Score = 50.0 bits (54), Expect = 0.014
 Identities = 35/40 (87%), Gaps = 0/40 (0%)
 Strand=Plus/Plus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATGGCaaaaa 2095
                |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct 20941542  TTGTTGTTGTTGTTGTTGTTGTTGTTGTTAAAAA 20941581
```

Features in this part of subject sequence:
 zinc finger/RING finger 2

Score = 44.6 bits (48), Expect = 0.62
 Identities = 48/64 (75%), Gaps = 0/64 (0%)
 Strand=Plus/Plus

```
Query 1143      CCCAGCGCCTCGGCCTCCGCCTCCTCGGCAGCCTCGGCCTCCGCAGCGCTCGCGGCCCGG 1202
                |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Sbjct 29814106  CCCAGCGCCTCCGCAGCGCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 29814165

Query 1203      GCGA 1206
                |||
Sbjct 29814166  CGCA 29814169
```

Features flanking this part of subject sequence:
 130830 bp at 5' side: T-box transcription factor TBX20 isoform B
 249206 bp at 3' side: HERPUD family member 2

Score = 44.6 bits (48), Expect = 0.62
 Identities = 30/34 (88%), Gaps = 0/34 (0%)
 Strand=Plus/Minus

```
Query 2423      CCTtttttCCTCCCTCTTTTCCCTTGCCCCCT 2456
                |||||  |||||  |||||  |||||  |||||  |||||
Sbjct 34913052  CCTTTTCTTCTCCTCCTCTTTTCTCTTCTCCTCT 34913019
```

Features flanking this part of subject sequence:
 627200 bp at 5' side: Sp8 transcription factor isoform 2
 15248 bp at 3' side: Sp4 transcription factor

Score = 42.8 bits (46), Expect = 2.2
 Identities = 35/42 (83%), Gaps = 2/42 (4%)
 Strand=Plus/Plus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG--GCaaaaa 2095
                |||||  |||  |||||  |||||  |||||  |||||  |||||
Sbjct 20941539  TTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTAAAAA 20941580
```

Features in this part of subject sequence:
 transformer-2 alpha

Score = 42.8 bits (46), Expect = 2.2
 Identities = 29/33 (87%), Gaps = 0/33 (0%)
 Strand=Plus/Plus

```
Query 766      CCAACTCCAGTCTCTCGGCCGCCGCCCTCTCCA 798
                |||  |||||  |||||  |||||  |||||  |||||
Sbjct 23034796  CCACCTCCACCTCCACCGGCCGCCGCCCTCTCCA 23034828
```

Features in this part of subject sequence:
 sorting nexin 8

Score = 41.0 bits (44), Expect = 7.5
 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

```
Query 1158      TCCGCTCCTCGGCAGCCTCGGCCTCCGCAGC 1189
                |||||  |||||  |||||  |||||  |||||
Sbjct 1842936  TCCGCTCCTCGTCAGCCTCCGCCTCAGCTGC 1842967
```

Features flanking this part of subject sequence:

213509 bp at 5' side: serine/threonine kinase 31 isoform b
 239342 bp at 3' side: neuropeptide Y

Score = 41.0 bits (44), Expect = 7.5
 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus

Query 2055 ATTGTTGTTATTGATGTTGTTGTTG 2079
 |||||
 Sbjct 23574476 ATTGTTGTTATTGTTGTTGTTGTTG 23574452

Features flanking this part of subject sequence:
 29183 bp at 5' side: ras related v-ral simian leukemia viral oncogene homolog A
 67365 bp at 3' side: hypothetical protein

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

Query 2053 TGATTGTTGTTATTGATGTTGTTGTTG 2079
 |||||
 Sbjct 39264011 TGATTGTTGTTGTTGTTGTTGTTGTTG 39263985

>ref|NT_010966.13|Hs18_11123 Homo sapiens chromosome 18 genomic contig, reference assembly
 Length=33548238

Features in this part of subject sequence:
 similar to hCG1790759

Score = 50.0 bits (54), Expect = 0.014
 Identities = 35/40 (87%), Gaps = 0/40 (0%)
 Strand=Plus/Minus

Query 2056 TTGTTGTTATTGATGTTGTTGTTGATGGC 2095
 |||||
 Sbjct 27513661 TTGTTGTTGTTGTTGTTGTTGTTGTTGAAAAA 27513622

>ref|NT_010393.15|Hs16_10550 Homo sapiens chromosome 16 genomic contig, reference assembly
 Length=25336229

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features flanking this part of subject sequence:
 508 bp at 5' side: ubiquitin specific protease 7
 128183 bp at 3' side: hypothetical protein LOC29035

Score = 50.0 bits (54), Expect = 0.014
 Identities = 54/70 (77%), Gaps = 5/70 (7%)
 Strand=Plus/Plus

Query 1142 TCCAGCGCCTCGGCCTCCGCCTCCTCGGCAGCCTC---GGCCTCC-GCAGCGCTCGCG 1196
 |||||
 Sbjct 370729 TCCGAGAGCCCGGCCTCCGCCTCCTCGGCCTCGCTCGGGGCTCCGGCAGCGGACGCG 370788

Query 1197 GCCCCGGGCA 1206
 |||||
 Sbjct 370789 GCGCCCGGCA 370798

Features in this part of subject sequence:
 poly(A)-specific ribonuclease (deadenylation nuclease)

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

Query 2052 GTGATTGTTGTTATTGATGTTGTTGTT 2078
 |||||
 Sbjct 5859015 GTGGTGTGTTATTGTTGTTGTTGTT 5858989

Features flanking this part of subject sequence:

```
Sort alignments for this subject seq
E value  Score  Percent identity
Query start position  Subject star
```

Score = 50.0 bits (54), Expect = 0.014
Identities = 35/40 (87%), Gaps = 0/40 (0%)
Strand=Plus/Minus

Features flanking this part of subject sequence:
 1351749 bp at 5' side: EGF-like repeats and discoidin I-like domains-containing ...
 881894 bp at 3' side: cytochrome c oxidase subunit VIIc precursor

Features flanking this part of subject sequence:
98714 bp at 5' side: interleukin 6 signal transducer isoform 2 precursor
25158 bp at 3' side: ankyrin repeat domain 55 isoform 1

```
Query 2049 CCTGTGATTGTTGTTATTGATGTTGTTGTTGATG 2082
          |||||
Spict 5965211 CCTGTG-TTGTGTTGTTGTTGTTGTTGTTGTTGTTG 5965179
```

```
>ref|NW_001838061.2|Hs12_WGA770_36 Homo sapiens chromosome 12 genomic contig, alternate as
(based on HuRef SCAF_1103279188362)
Length=32873191
```

```
Sort alignments for this subject seq
E value  Score  Percent identity
Query start position  Subject star
```

Features flanking this part of subject sequence:
63961 bp at 5' side: hypothetical protein LOC196477
1181244 bp at 3' side: hypothetical protein

Score = 46.4 bits (50), Expect = 0.18
Identities = 34/40 (85%), Gaps = 0/40 (0%)
Strand=Plus/Plus

Query	2056	TTGTTGTTATTGATGTTGTTGTTGATGGC	2095
Spict	18088785	TTGTTGTTGTTGTTGTTGTTGTTGTTTAAAAA	18088824

Features flanking this part of subject sequence:
4678 bp at 5' side: damage-regulated autophagy modulator
42189 bp at 3' side: N-acetylglucosamine-1-phosphate transferase

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```
Query    2056      TTGTTGTTATTGATGTTGTTGTTGATG      2082
          |||||
Subject  7113244   TTGTTGTTATTGTTGTTGTTGTTGTTG    7113270
```

Features flanking this part of subject sequence:
 15027 bp at 5' side: IKK interacting protein isoform 1
 9365 bp at 3' side: solute carrier family 25 member 3 isoform b precursor

Score = 41.0 bits (44), Expect = 7.5
 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

```
Query   2051      TGTGATTGTTGTTATTGATGTTGTTGTTGATG   2082
          ||||| ||||| ||| ||||| ||||| |||
Sbjct   10374017  TGTGTTTGTGTGTGTGTGTGTGTGTGTGTGTG   10374048
```

Features flanking this part of subject sequence:
 11252 bp at 5' side: tetraspanin 19
 111109 bp at 3' side: solute carrier family 6, member 15 isoform 1

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

```
Query   2059      TTGTTATTGATGTTGTTGTTGATGGCA   2085
          ||||| ||| ||||| ||||| ||||| |||
Sbjct   23985705  TTGTGTGTGTGTGTGTGTGTGTGTGTGTG   23985679
```

Features flanking this part of subject sequence:
 1244859 bp at 5' side: solute carrier family 6, member 15 isoform 2
 505592 bp at 3' side: transmembrane and tetratricopeptide repeat containing 2


Score = 41.0 bits (44), Expect = 7.5
 Identities = 29/32 (90%), Gaps = 1/32 (3%)
 Strand=Plus/Minus

```
Query   2049      CCTGT-GATTGTTGTTATTGATGTTGTTGTTG   2079
          ||||| | ||||| ||||| ||||| |||||
Sbjct   25350079  CCTGTAGTTGTGTGTATTGTTGTGTGTGTGTG   25350048
```

Features flanking this part of subject sequence:
 60181 bp at 5' side: hypothetical protein
 36799 bp at 3' side: synaptotagmin I

Score = 41.0 bits (44), Expect = 7.5
 Identities = 27/30 (90%), Gaps = 0/30 (0%)
 Strand=Plus/Minus

```
Query   2053      TGATTGTGTTATTGATGTTGTTGTTGATG   2082
          || ||||| ||| ||| ||||| ||||| |||
Sbjct   29504024  TGTTGTGTGTGTGTGTGTGTGTGTGTGTG   29503995
```

>ref|NW_001838006.2|Hs10_WGA715_36  Homo sapiens chromosome 10 genomic contig, alternate as
 (based on HuRef SCAF_1103279188397)
 Length=24511762

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features flanking this part of subject sequence:
 21875 bp at 5' side: VPS10 domain receptor protein SORCS 3
 164826 bp at 3' side: coiled-coil domain containing 147

Score = 46.4 bits (50), Expect = 0.18
 Identities = 28/30 (93%), Gaps = 0/30 (0%)
 Strand=Plus/Plus

```
Query   2050      CTGTGATTGTTGTTATTGATGTTGTTGTTG   2079
          ||||| ||||| ||| ||| ||||| ||||| |||
Sbjct   18620835  CTGTGATTGTTGTTGTTGTTGTTGTTGTTG   18620864
```

Features in this part of subject sequence:
 attractin-like 1

Score = 42.8 bits (46), Expect = 2.2
 Identities = 31/36 (86%), Gaps = 0/36 (0%)
 Strand=Plus/Plus

```

Query    2047      GACCTGTGATTGTTGTTATTGATGTTGTTGTTGATG    2082
          |||||  ||  |||||  ||  |||||  ||  |||||  ||
Sbjct    7796118    GACCTATGCTTGTGTTGTTGTTGTTGTTGTTGTTG    7796153

```

Features in this part of subject sequence:
eukaryotic translation initiation factor 3, subunit 10 th...

Score = 41.0 bits (44), Expect = 7.5
Identities = 30/34 (88%), Gaps = 1/34 (2%)
Strand=Plus/Plus

```

Query    2049      CCGTGTGATTGTTGTTATTGATGTTGTTGTTGATG    2082
          |||||  |||||  ||  ||  |||||  ||  |||||  ||
Sbjct    4199496    CCGTGTG-TTGTTGTTTTGTTGTTGTTGTTGTTG    4199528

```

>ref|NW_001838988.2|Hs6_WGA381_36 Homo sapiens chromosome 6 genomic contig, alternate asse
(based on HuRef SCAF_1103279187031)
Length=10950630

Features flanking this part of subject sequence:
5780 bp at 5' side: PR domain containing 13
31753 bp at 3' side: cyclin C isoform a

Score = 46.4 bits (50), Expect = 0.18
Identities = 30/32 (93%), Gaps = 1/32 (3%)
Strand=Plus/Minus

```

Query    2423      CCtttt-tttCCTCCCTCTTTTCCCTTGCCCC    2453
          |||||  ||||  |||||  |||||  |||||  |||||
Sbjct    6415009    CCTTTATTTCCTCCCTCTTTTCCCTTGCCCC    6414978

```

>ref|NT_025741.14|Hs6_25897 Homo sapiens chromosome 6 genomic contig, reference assembly
Length=61645385

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features flanking this part of subject sequence:
39819 bp at 5' side: cyclin C isoform b
5780 bp at 3' side: PR domain containing 13

Score = 46.4 bits (50), Expect = 0.18
Identities = 30/32 (93%), Gaps = 1/32 (3%)
Strand=Plus/Plus

```

Query    2423      CCtttt-tttCCTCCCTCTTTTCCCTTGCCCC    2453
          |||||  ||||  |||||  |||||  |||||  |||||
Sbjct    4218557    CCTTTATTTCCTCCCTCTTTTCCCTTGCCCC    4218588

```

Features flanking this part of subject sequence:
44704 bp at 5' side: cell division cycle 2-like 6 (CDK8-like)
15240 bp at 3' side: S-adenosylmethionine decarboxylase 1 isoform 1 precursor

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```

Query    2056      TTGTTGTTATTGATGTTGTTGTTGATG    2082
          |||||  |||||  |||||  |||||  |||||  ||
Sbjct    15350472    TTGTTGTTGTTGATGTTGTTGTTGTTGTTG    15350498

```

Features flanking this part of subject sequence:
536408 bp at 5' side: connexin 43
415307 bp at 3' side: heat shock transcription factor 2

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```

Query    2056      TTGTTGTTATTGATGTTGTTGTTGATG    2082
          |||||  ||||  |||||  |||||  |||||  ||

```

Sbjct 26409985 TTGTTGTTGTTGTTGTTGTTGTTGATG 26410011

Features flanking this part of subject sequence:

422057 bp at 5' side: sterile alpha motif domain containing 5
356529 bp at 3' side: SAM and SH3 domain containing 1


Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

Query 2237 CTITGTTTTGTTTTATTTTGCITCTTG 2263
||| ||||| ||||| ||||| ||||| |||||
Sbjct 52412078 CTTTGTGTTGTTTATTTTGCITTTTG 52412104

Features in this part of subject sequence:
opioid receptor, mu 1 isoform MOR-10
phosphoinositide-binding protein PIP3-E

Score = 41.0 bits (44), Expect = 7.5
Identities = 29/32 (90%), Gaps = 1/32 (3%)
Strand=Plus/Minus

Query 2056 TTGTTGTTATTGATGTTGTTGTTGATGGCAA 2087
||||||| ||| ||||| ||||| ||||| |||||
Sbjct 58617258 TTGTTGTTGTTGTTGTTGTTGTTGA-GGCAA 58617228


>ref|NT_113898.1|Hs6_111617  Homo sapiens chromosome 6 genomic contig, reference assembly
Length=1305230

Features flanking this part of subject sequence:

539 bp at 5' side: similar to HGC6.4
105 bp at 3' side: similar to myeloid/lymphoid or mixed-lineage leukemia (tr...

Score = 46.4 bits (50), Expect = 0.18
Identities = 31/35 (88%), Gaps = 0/35 (0%)
Strand=Plus/Minus

Query 1155 GCCTCCGCCCTCCTCGGCAGCCTCGGCCTCCGCAGC 1189
||||||| ||||| ||||| ||||| ||||| |||||
Sbjct 814424 GCCTCCGCCCTCCTCGGCAGCCTCGGCCTCCGCAGC 814390


>ref|NT_007302.13|Hs6_7459  Homo sapiens chromosome 6 genomic contig, reference assembly
Length=2236975

Features flanking this part of subject sequence:

539 bp at 5' side: hypothetical protein LOC653483
105 bp at 3' side: myeloid/lymphoid or mixed-lineage leukemia (trithorax hom...

Score = 46.4 bits (50), Expect = 0.18
Identities = 31/35 (88%), Gaps = 0/35 (0%)
Strand=Plus/Minus

Query 1155 GCCTCCGCCCTCCTCGGCAGCCTCGGCCTCCGCAGC 1189
||||||| ||||| ||||| ||||| ||||| |||||
Sbjct 185635 GCCTCCGCCCTCCTCGGCAGCCTCGGCCTCCGCAGC 185601

>ref|NT_030059.12|Hs10_30314  Homo sapiens chromosome 10 genomic contig, reference assembly
Length=44617998

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features flanking this part of subject sequence:

164871 bp at 5' side: coiled-coil domain containing 147
21898 bp at 3' side: VPS10 domain receptor protein SORCS 3

Score = 46.4 bits (50), Expect = 0.18
Identities = 28/30 (93%), Gaps = 0/30 (0%)
Strand=Plus/Minus

```

Query    2050      CTGTGATTGTTGTTATTGATGTTGTTGTTG  2079
          |||
Sbjct    25127714   CTGTGATTGTTGTTGTTGTTGTTGTTGTTG  25127685

```

Features in this part of subject sequence:
 attractin-like 1

Score = 42.8 bits (46), Expect = 2.2
 Identities = 31/36 (86%), Gaps = 0/36 (0%)
 Strand=Plus/Minus

```

Query    2047      GACCTGTGATTGTTGTTATTGATGTTGTTGATG  2082
          |||||
Sbjct    35956938   GACCTATGCTTGTGTTGTTGTTGTTGTTGTTGTTG  35956903

```

Features flanking this part of subject sequence:
 48094 bp at 5' side: protein phosphatase 1, regulatory (inhibitor) subunit 3C
 117589 bp at 3' side: tankyrase, TRF1-interacting ankyrin-related ADP-ribose po...

Score = 41.0 bits (44), Expect = 7.5
 Identities = 33/40 (82%), Gaps = 0/40 (0%)
 Strand=Plus/Plus

```

Query    2043      GGGCGACCTGTGATTGTTGTTATTGATGTTGTTGTTGATG  2082
          |||||
Sbjct    12189336   GGGCTTCCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG  12189375

```

Features in this part of subject sequence:
 eukaryotic translation initiation factor 3, subunit 10 th...

Score = 41.0 bits (44), Expect = 7.5
 Identities = 30/34 (88%), Gaps = 1/34 (2%)
 Strand=Plus/Minus

```

Query    2049      CCTGTGATTGTTGTTATTGATGTTGTTGTTGTTGATG  2082
          |||||
Sbjct    39551677   CCTGTG-TTGTGTTTTTGTGTTGTTGTTGTTGTTGTTGTTG  39551645

```

>ref|NW_001838769.1|Hs2_WGA162_36 Homo sapiens chromosome 2 genomic contig, alternate asse
 (based On HuRef SCAF_1103279188433)
 Length=57109151

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features in this part of subject sequence:
 neurexin 1 isoform alpha precursor

Score = 44.6 bits (48), Expect = 0.62
 Identities = 26/27 (96%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

```

Query    2053      TGATTGTTGTTATTGATGTTGTTGTTG  2079
          |||
Sbjct    20778224   TGATTGTTGTTATTGTTGTTGTTGTTGTTG  20778198

```

Features in this part of subject sequence:
 hypothetical protein

Score = 42.8 bits (46), Expect = 2.2
 Identities = 66/91 (72%), Gaps = 9/91 (9%)
 Strand=Plus/Plus

```

Query    1277      GGGCGGCGTGGGCGCGGGAGCCGAC--CCCAGCGACCCCTGGGCGCTACGAGGAGGAG  1334
          |||
Sbjct    7734878   GGGCGGCGCGGG-GCGGG-GCCGGCGGCGGGGACTCACTGGGCGG-----GGCGGAG  7734930
Query    1335      GGC GCGGGCTGCTCGCCCGACGCGCCAGCC  1365
          |||
Sbjct    7734931   GGC GCGGGGACGCGGGGCGGACCTCCAGCC  7734961

```

Features in this part of subject sequence:
sterolin 1

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```
Query   2056      TTGTTGTTATTGATGTTGTTGTTGATG   2082
          |||
Sbjct   13885678  TTGTTGTTATTGTTGTTGTTGTTGTTG   13885704
```

Features flanking this part of subject sequence:
23818 bp at 5' side: M-phase phosphoprotein 10
14630 bp at 3' side: poly(A) binding protein interacting protein 2B


Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Minus

```
Query   2056      TTGTTGTTATTGATGTTGTTGTTGATG   2082
          |||
Sbjct   41233894  TTGTTGTTATTGTTGTTGTTGTTGCTG   41233868
```

Features flanking this part of subject sequence:
16873 bp at 5' side: STAM binding protein
23234 bp at 3' side: actin, gamma 2 propeptide

Score = 41.0 bits (44), Expect = 7.5
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Minus

```
Query   2056      TTGTTGTTATTGATGTTGTTGTTGA   2080
          |||
Sbjct   43937347  TTGTTGTTATTGTTGTTGTTGTTGA   43937323
```

>ref|NW_001838115.2|Hs14_WGA824_36  Homo sapiens chromosome 14 genomic contig, alternate as
(based on HuRef SCAF_1103279188327)
Length=8970161

Sort alignments for this subject seq
E value Score Percent identity
Query start position Subject star

Features in this part of subject sequence:
REST corepressor 1


Score = 44.6 bits (48), Expect = 0.62
Identities = 35/42 (83%), Gaps = 0/42 (0%)
Strand=Plus/Minus

```
Query   1148      CGCCTCGGCCTCCGCCCTCCTCGGCAGCCTCGGCCTCCGCAGC   1189
          |||
Sbjct   1645733  CGCCTCGGGCGCGCGCCCTCCTCAGCCTCGGCCTCGGCCTCCGC   1645692
```

Features flanking this part of subject sequence:
73361 bp at 5' side: SET domain containing 3 isoform b
65304 bp at 3' side: B-cell CLL/lymphoma 11B isoform 2

Score = 41.0 bits (44), Expect = 7.5
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Minus

```
Query   2056      TTGTTGTTATTGATGTTGTTGTTGA   2080
          |||
Sbjct   4895427  TTGTTGTTATTGTTGTTGTTGTTGA   4895403
```

>ref|NW_001838461.1|Hs18_WGA1170_36  Homo sapiens chromosome 18 genomic contig, alternate a
(based on HuRef SCAF_1103279188344)
Length=10560353

Features flanking this part of subject sequence:

52573 bp at 5' side: zinc finger protein 161 homolog
 48166 bp at 3' side: erythrocyte membrane protein band 4.1-like 3

Score = 44.6 bits (48), Expect = 0.62
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus

```
Query 2050      CTGTGATTGTTGTTATTGATGTTGTTGTTGAT 2081
                ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 5299965   CTGTGTTGTTGTTATTGTTGTTGTTGTTGAT 5299934
```

>ref|NW_001838768.1|Hs2_WGA161_36 Homo sapiens chromosome 2 genomic contig, alternate asse
 (based on HuRef SCAF_1103279188306)
 Length=8993619

Features flanking this part of subject sequence:

9750 bp at 5' side: similar to hCG1783917
 35597 bp at 3' side: ATPase family, AAA domain containing 2B

Score = 44.6 bits (48), Expect = 0.62
 Identities = 35/42 (83%), Gaps = 0/42 (0%)
 Strand=Plus/Plus

```
Query 2041      AGGGGCGACCTGTGATTGTTGTTATTGATGTTGTTGATG 2082
                ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 2769192   AGGTGGGACCTTCATTGTTGTTGTTGTTGTTGTTGTTG 2769233
```

>ref|NW_001838987.1|Hs6_WGA380_36 Homo sapiens chromosome 6 genomic contig, alternate asse
 (based on HuRef SCAF_1103279188274B)
 Length=25130961

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features flanking this part of subject sequence:

673617 bp at 5' side: similar to OITHUMP00000016822
 14999 bp at 3' side: similar to hCG1652647

Score = 44.6 bits (48), Expect = 0.62
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

```
Query 2056      TTGTTGTTATTGAIGTTGTTGTTGATGGCAA 2087
                ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 16521782   TTGTTGTTATTGTTGTTGTTGTTGTTGTTGTTGTTG 16521813
```

Features flanking this part of subject sequence:

877536 bp at 5' side: hypothetical protein
 56773 bp at 3' side: similar to PRO2122

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

```
Query 2056      TTGTTGTTATTGAIGTTGTTGTTGATG 2082
                ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 11600965   TTGTTGTTATTGTTGTTGTTGTTGTTGTTGTTGTTG 11600939
```

>ref|NW_001838928.2|Hs5_WGA321_36 Homo sapiens chromosome 5 genomic contig, alternate asse
 (based on HuRef SCAF_1103279188369)
 Length=3866709

Features flanking this part of subject sequence:

318147 bp at 5' side: cadherin 18, type 2 preproprotein
 1493882 bp at 3' side: hypothetical protein

Score = 44.6 bits (48), Expect = 0.62
 Identities = 26/27 (96%), Gaps = 0/27 (0%)
 Strand=Plus/Plus

```
Query 2056      TTGTTGTTATTGATGTTGTTGTTGATG 2082
```

Sbjct 2312131 |||||
 TTGTTGTTATTGATGTTGTTGTTG 2312157

>ref|NW_001838915.1|Hs4_WGA308_36 Homo sapiens chromosome 4 genomic contig, alternate asse
 (based on HuRef SCAF_1103279188399)
 Length=43867763

Sort alignments for this subject seq
 E value Score Percent identity
 Query start position Subject star

Features in this part of subject sequence:

calcium/calmodulin-dependent protein kinase II delta isof...
 calcium/calmodulin-dependent protein kinase II delta isof...

Score = 44.6 bits (48), Expect = 0.62
 Identities = 29/32 (90%), Gaps = 0/32 (0%)
 Strand=Plus/Minus

Query 2051 TGIGATTGTTGTTATTGATGTTGTTGTTGAIG 2082
 ||| |||||
 Sbjct 38913468 TGTATTGTTGTTATTGTTGTTGTTGTTGTTG 38913437

Features flanking this part of subject sequence:

133705 bp at 5' side: protein kinase, cGMP-dependent, type II
 89301 bp at 3' side: RasGEF domain family, member 1B

Score = 41.0 bits (44), Expect = 7.5
 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Plus

Query 2051 TGIGATTGTTGTTATTGATGTTGTTGTTGAIG 2082
 |||||
 Sbjct 6765249 TGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 6765280

Features in this part of subject sequence:
 kelch-like 8

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Plus

Query 2053 TGATTGTTGTTATTGATGTTGTTGTTG 2079
 ||| |||||
 Sbjct 12614178 TGAGTGTGTTATTGTTGTTGTTGTTG 12614204

Features flanking this part of subject sequence:

29889 bp at 5' side: protein phosphatase 1K (PP2C domain containing)
 70965 bp at 3' side: hect domain and RLD 6

Score = 41.0 bits (44), Expect = 7.5
 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Plus

Query 2055 ATTGTTGTTATTGATGTTGTTGTTG 2079
 |||||
 Sbjct 13742614 ATTGTTGTTATTGTTGTTGTTGTTG 13742638

Features flanking this part of subject sequence:

278276 bp at 5' side: hypothetical protein
 1070253 bp at 3' side: hypothetical protein LOC132720

Score = 41.0 bits (44), Expect = 7.5
 Identities = 24/25 (96%), Gaps = 0/25 (0%)
 Strand=Plus/Minus

Query 2055 ATTGTTGTTATTGATGTTGTTGTTG 2079
 |||||
 Sbjct 36489587 ATTGTTGTTATTGATGCTGTTGTTG 36489563

Features flanking this part of subject sequence:

7/16/08

calcium/calmodulin-dependent protein kinase II delta isof...
calcium/calmodulin-dependent protein kinase II delta isof...

Score = 44.6 bits (48), Expect = 0.62
Identities = 29/32 (90%), Gaps = 0/32 (0%)
Strand=Plus/Minus

Query 2051 TGIGATTGTTGTTATTGATGTTGTTGTTGATG 2082
||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 38971724 TGTATTGTTGTTATTGTTGTTGTTGTTGTTG 38971693

Features flanking this part of subject sequence:
133593 bp at 5' side: protein kinase, cGMP-dependent, type II
89097 bp at 3' side: RasGEF domain family, member 1B

Score = 41.0 bits (44), Expect = 7.5
Identities = 28/32 (87%), Gaps = 0/32 (0%)
Strand=Plus/Plus

Query 2051 TGIGATTGTTGTTATTGATGTTGTTGTTGATG 2082
||| ||||| ||||| ||| ||||| ||||| |||
Sbjct 6807515 TGTGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 6807546

Features in this part of subject sequence:
kelch-like 8

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

Query 2053 TGATTGTTGTTATTGATGTTGTTGTTG 2079
||| ||||| ||||| ||||| ||||| |||||
Sbjct 12656097 TGAGTGTGTTGTTATTGTTGTTGTTGTTG 12656123

Features flanking this part of subject sequence:
29879 bp at 5' side: protein phosphatase 1K (PP2C domain containing)
70436 bp at 3' side: hect domain and RLD 6

Score = 41.0 bits (44), Expect = 7.5
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Plus

Query 2055 ATTGTTGTTATTGATGTTGTTGTTGTTG 2079
||| ||||| ||||| ||||| ||||| |||||
Sbjct 13777335 ATTGTTGTTATTGTTGTTGTTGTTGTTG 13777359

Features in this part of subject sequence:
hypothetical protein LOC54848

Score = 41.0 bits (44), Expect = 7.5
Identities = 28/32 (87%), Gaps = 0/32 (0%)
Strand=Plus/Plus

Query 2056 TTGTTGTTATTGATGTTGTTGTTGATGGCAA 2087
|| ||||| ||| ||||| ||||| ||||| |||||
Sbjct 31046853 TTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 31046884

Features flanking this part of subject sequence:
278486 bp at 5' side: hypothetical protein
1070062 bp at 3' side: hypothetical protein LOC132720

Score = 41.0 bits (44), Expect = 7.5
Identities = 24/25 (96%), Gaps = 0/25 (0%)
Strand=Plus/Minus

Query 2055 ATTGTTGTTATTGATGTTGTTGTTGTTG 2079
||| ||||| ||||| ||||| ||||| |||||
Sbjct 36544821 ATTGTTGTTATTGATGCTGTTGTTGTTG 36544797

Features in this part of subject sequence:
ankyrin 2 isoform 1

ankyrin 2 isoform 2

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

Query 2056 TTGTTGTTATTGATGTTGTTGTTGATG 2082
 |||||
 Sbjct 38574052 TTGTTGTTATTGTTGTTGTTGTTGTTG 38574026

Features flanking this part of subject sequence:
 82203 bp at 5' side: translocation associated membrane protein 1-like 1
 140285 bp at 3' side: N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3

Score = 41.0 bits (44), Expect = 7.5
 Identities = 27/30 (90%), Gaps = 0/30 (0%)
 Strand=Plus/Plus

Query 2053 TGATTGTTGTTATTGATGTTGTTGTTGATG 2082
 |||||
 Sbjct 43382897 TGTGTTGTTGTTATTGTTGTTGTTGTTGCTG 43382926

Features flanking this part of subject sequence:
 859109 bp at 5' side: hypothetical protein
 1066931 bp at 3' side: hypothetical protein

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

Query 2056 TTGTTGTTATTGATGTTGTTGTTGATG 2082
 |||||
 Sbjct 56126973 TTGTTGTTGTTGTTGTTGTTGTTGATG 56126947

Features flanking this part of subject sequence:
 323925 bp at 5' side: protocadherin 10 isoform 2 precursor
 1467518 bp at 3' side: similar to Ubiquinol-cytochrome c reductase, complex III ...

Score = 41.0 bits (44), Expect = 7.5
 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Minus

Query 2051 TGTGATTGTTGTTATTGATGTTGTTGTTGATG 2082
 |||||
 Sbjct 58946089 TGTGATTGTTGTTGTTGTTGTTGTTGTTGTTG 58946058

Features in this part of subject sequence:
 similar to FRAS1-related extracellular matrix protein 3

Score = 41.0 bits (44), Expect = 7.5
 Identities = 25/27 (92%), Gaps = 0/27 (0%)
 Strand=Plus/Minus

Query 2056 TTGTTGTTATTGATGTTGTTGTTGATG 2082
 |||||
 Sbjct 69094402 TTGTTGTTGTTGATGTTGTTGTTGTTGTTG 69094376

Features flanking this part of subject sequence:
 39101 bp at 5' side: peptidylprolyl isomerase D
 6793 bp at 3' side: hypothetical protein LOC57600

Score = 41.0 bits (44), Expect = 7.5
 Identities = 28/32 (87%), Gaps = 0/32 (0%)
 Strand=Plus/Minus

Query 2051 TGTGATTGTTGTTATTGATGTTGTTGTTGATG 2082
 |||||
 Sbjct 84231719 TGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 84231688

Features flanking this part of subject sequence:
 462638 bp at 5' side: membrane-associated RING-CH protein I

Features in this part of subject sequence:

adenylate kinase 5 isoform 1
adenylate kinase 5 isoform 2

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```
Query   2053      TGATTGTTGTTATTGATGTTGTTGTTG   2079
          || |||||
Sbjct   47884298  TGTGTTGTTGTTATTGTTGTTGTTGTTG   47884324
```

Features flanking this part of subject sequence:

20976 bp at 5' side: guanylate binding protein 1, interferon-inducible, 67kD
23939 bp at 3' side: guanylate binding protein 2, interferon-inducible

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Minus


```
Query   2056      TTGTTGTTATTGATGTTGTTGTTGATG   2082
          |||||
Sbjct   59521838  TTGTTGTTATTGTTGTTGTTGTTGTTG   59521812
```

Features flanking this part of subject sequence:

1219349 bp at 5' side: similar to hCG2040669
184274 bp at 3' side: polypyrimidine tract binding protein 2

Score = 41.0 bits (44), Expect = 7.5
Identities = 25/27 (92%), Gaps = 0/27 (0%)
Strand=Plus/Plus

```
Query   2056      TTGTTGTTATTGATGTTGTTGTTGATG   2082
          |||||
Sbjct   66975040  TTGTTGTTATTGTTGTTGTTGTTGTTG   66975066
```

>ref|NT_010859.14|Hs18_11016  Homo sapiens chromosome 18 genomic contig, reference assembly
Length=15400898

Features flanking this part of subject sequence:

37804 bp at 5' side: hypothetical protein
48190 bp at 3' side: erythrocyte membrane protein band 4.1-like 3

Score = 44.6 bits (48), Expect = 0.62
Identities = 29/32 (90%), Gaps = 0/32 (0%)
Strand=Plus/Minus

```
Query   2050      CTGIGATTGTTGTTATTGATGTTGTTGTTGAT   2081
          |||||
Sbjct   5336492  CTGTTGTTGTTGTTATTGTTGTTGTTGTTGAT   5336461
```

Database: human build 36.3 reference assembly genomic scaffolds

Posted date: Apr 16, 2008 7:40 PM

Number of letters in database: 1,523,044,440

Number of sequences in database: 49,942

Lambda	K	H
0.634	0.408	0.912

Lambda	K	H
0.634	0.408	0.912

Matrix: blastn matrix:2 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 49942

Number of Hits to DB: 5820376

Number of extensions: 423311

Number of successful extensions: 1102

Number of sequences better than 10: 52
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 1085
Number of HSP's successfully gapped: 58
Length of query: 2797
Length of database: 5818011736
Length adjustment: 35
Effective length of query: 2762
Effective length of database: 5816263766
Effective search space: 16064520521692
Effective search space used: 16064520521692
A: 0
X1: 22 (20.1 bits)
X2: 33 (29.8 bits)
X3: 110 (99.2 bits)
S1: 36 (33.7 bits)
S2: 44 (41.0 bits)

